



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 182745

TO: Pablo Whaley
Location: rem/4C35/2C70
Art Unit: 1631
Friday, March 24, 2006
Case Serial Number: 10/509595

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523
toby.port@uspto.gov

Search Notes

Examiner Whaley,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2006, 01:14:39 ; Search time 28911 Seconds
(without alignments)
11796.918 Million cell updates/sec

Title: SEQ1-4037A

Perfect score: 6000
Sequence: 1 gccccacaggaagctctcccc.....atcaggggaagctatgtac 6000

Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sas:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5998.4	99.9	79376	8	HS454G6
2	5972	99.5	170425	14	AC0024490
3	4888.8	81.5	6169	6	AR123665
4	4888.8	81.5	6169	6	BD065041
5	4888.8	81.5	6169	6	BD237936
6	4888.8	81.5	6169	6	AR242746
7	4069.4	67.8	5300	6	AR123663
8	4069.4	67.8	5300	6	BD237934
9	4069.4	67.8	5300	6	AR242744
10	4068.4	67.8	5299	6	BD065039
11	4057.4	67.6	5304	6	AR123664
12	4057.4	67.6	5304	6	BD065040
13	4057.4	67.6	5304	6	BD237935
14	4057.4	67.6	5304	6	AR242745
15	4044.8	67.4	5300	8	AF007562
16	4015.8	66.9	5271	6	BD237961
17	4015.8	66.9	5271	6	AR242771
18	2773.4	46.2	2800	6	BD225246

19	2773.4	46.2	2800	6	AR212944	AR212944 Sequence
20	2773.4	46.2	2800	6	AR532546	AR532546 Sequence
21	2773.4	46.2	2800	8	HSWYOC1	AF049791 Homo sapi
22	1225.2	20.4	3163	8	AB006688	AB006688 Homo sapi
23	1068.8	17.8	1086	8	HSGLC1A1	Z97171 Homo sapien
24	1043.8	17.4	1311	8	AY190128S1	AY190128 Macaca fa
25	770	12.8	2166	6	AR163678	AR163678 Sequence
26	770	12.8	2166	6	BD009308	BD009308 G1aucoma-
27	677.8	11.3	2145	6	AX300008	AX300008 Sequence
28	664.4	11.1	2111	8	BC029261	BC029261 Homo sapi
29	651.2	10.9	1934	8	D88214	D88214 Homo sapien
30	640.4	10.7	1548	6	AR123668	AR123668 Sequence
31	640.4	10.7	1548	6	BD065064	BD065064 Methods f
32	640.4	10.7	1548	6	BD237959	BD237959 Nucleic a
33	640.4	10.7	1548	6	AR242769	AR242769 Sequence
34	640.4	10.7	1871	6	AX004457	AX004457 Sequence
35	640.4	10.7	1871	6	AX004474	AX004474 Sequence
36	640.4	10.7	1999	6	AR030962	AR030962 Sequence
37	640.4	10.7	1999	6	AR066022	AR066022 Sequence
38	640.4	10.7	1999	6	AR069089	AR069089 Sequence
39	640.4	10.7	2002	8	HSU85257	U85257 Human trade
40	640.4	10.7	2002	6	A84847	A84847 Sequence 2
41	635.6	10.6	2000	6	A84850	A84850 Sequence 2
42	626.4	10.4	2045	6	CQ726274	CQ726274 Sequence
43	626.4	10.4	2061	8	HSAP001620	AF001620 Homo sapi
44	626	10.4	23704	9	AF289236	AF289236 Mus muscu
45	626	10.4	188661	9	AC138218	AC138218 Mus muscu

ALIGNMENTS

RESULT 1
HS454G6/c
LOCUS
DEFINITION
Human DNA sequence from clone RP3-454G6 on chromosome 1q24 contains the 3' end of the gene for HBxAg transactivated protein 2 (XTP2) and the MYOC gene for myocilin, trabecular meshwork inducible glucocorticoid response, complete sequence.

ACCESSION
Z98750
VERSION
Z98750.1 GI:2887277
KEYWORDS
HTG; glucocorticoid; HBxAg; MYOC; myocilin; transactivated protein 2; XTP2.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 79376)
Pavitt, R.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Feb 14, 1998 this sequence version replaced gi:2465060.

COMMENT

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMBEP; Information on the WORMBEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP3-454G6 is from the library RP3-3 constructed by the group of P. J. Pater de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCVPAC2

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers

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FEATURES
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    /clone_id="RPCI-3"
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Query Match 99.9%; Score 5998.4; DB 8; Length 79376;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCCACAGGAAGTCTCCCACTCTAGACTTGTGACATCAGAGTTTACAGCCAGAAAGTTC 60
DB 67191 GCTCCACAGGAAGTCTCCCACTCTAGACTTGTGACATCAGAGTTTACAGCCAGAAAGTTC 67132
QY 61 CGTAGAGGTGAGGGTCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTCACTGC 120
DB 67131 CGTAGAGGTGAGGGTCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTCACTGC 67072
QY 121 AACCTCTGCTCCCAAGTTCAGCAATTCCTCTGTCTCAGCTCCCGCGTACGCTGGAGT 180
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QY 181 ACAGGCGCAGCGCCGCTATTTTGTATTTGTAAGAGATGGGGTTTCAACATATTAG 240
DB 67011 ACAGGCGCAGCGCCGCTATTTTGTATTTGTAAGAGATGGGGTTTCAACATATTAG 66952
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DB 66951 CCCGCTGTCTTGAATCTCTGACCTCAGGTGATCCACCACCTCAGCTCTTAAGTGC 66892
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 Homiidae; Homo.
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 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens chromosome 1, clone RP11-138F3
 JOURNAL Unpublished

REFERENCE
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 Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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 Zody, M.

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Web site: <http://www-seq.wi.mit.edu>

Project Information
 Contact: sequence.submissions@genome.wi.mit.edu

Center project name: L7153
 Center clone name: 138_F_3

Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731
 Consensus quality: 151483 bases at least Q40
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 Consensus quality: 164708 bases at least Q20

Insert size: 167000; agarose-fp
 Quality coverage: 4.1 in Q20 bases; sum-of-coverage
 Quality coverage: 4.1 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently
 consists of 28 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

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OY	1141	AATGTCTGTGTGATCTGAGCTGTGAGACTCTCTTGGCTTCAGGCTTCAGAAAGAAATGG	1200
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OY	1441	CTGCTTGAAGAGAAAGATCTATTTCATGAAAGGAGTCAAGTTTCAATAAGCTGAGCTTT	1500
Db	66345	CTGCTTGAAGAGAAAGATCTATTTCATGAAAGGAGTCAAGTTTCAATAAGCTGAGCTTT	66404
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Db 66885 CAATGCTTCAGAAAGCTCAATGAACCCAAAGCAGCAATTTCTTCCCTAAGCATAGC 66944
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Db 66945 AATGCAATTTGCAATTAACCAAAAGATGACAGACTAATCTGTGTGATGCTTTGCTG 67004
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QY	3841	GTAAGGTGCATTAATTTGGATGTTCTTTTAAAAAGAACTCCAAACAGACTTCGAA	3900
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Dp	70005	TGTTAAATAGACCTTTATTTTATGAATTAACAATAGATTTGGAAATGATTAATAGTGTA	70064
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Dp	70065	AGTTTTGTATTTTAAATGTTCTTCCCTGGCAAAATAAAGATGGACCTCTGT	70124
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Dp	70365	AGTGGGCTCCCAATATATCCCTGTGAGGAAGTGTCTATATGATGAGAAATTAACAAGC	70424
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Dp	70485	GAAAAAAGGGGTGGGGAAGGGCTGTCTATATTTAAAGACTAAAGAAATGTGTAACC	70544
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Dp	70545	AAATGTAGTGCATGAGTCTTGAATGTGTCTTCAATCCAAAGGGGGAAAAAGGCTATAGAGA	70604
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Db	70785	TTGAGAAAGACCTGCAAAATATATATGATTAATGAGAGAAAGAAAGCTAAACCAACTGTGGCA	70844
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JOURNAL	Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders		
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Matches 4949; Conservative	0; Mismatches	2; Indels	9; Gaps
5;			
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Qy	61	CGTAGAGGTGAGGGGTCTGTGCTTAACACTACCTGTATGCTCTACACCTGAGCTCACTGC	120
Db	1276	CGTAGAGGTGAGGGGTCTGTGCTTAACACTACCTGTATGCTCTACACCTGAGCTCACTGC	1335
Qy	121	AACCTCTGCTCCAGGTTCAAGCAATTCCTCTCTCAGCCTCCCGGTAAGCTGGGACT	180
Db	1336	AACCTCTGCTCCAGGTTCAAGCAATTCCTCTCTCAGCCTCCCGGTAAGCTGGGACT	1395
Qy	181	ACAGGCGCACCGCCGGCTAATTTTTTGTATTTGTATGTAAGATGGGGTTTACACATATTAG	240
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Qy	241	CCCGGCTGCTTGAACCTCGTACCTCAGGATGATCCACCACTCAGCCTCCCTAAAGTGC	300
Db	1456	CCCGGCTGCTTGAACCTCGTACCTCAGGATGATCCACCACTCAGCCTCCCTAAAGTGC	1515
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Qy	481	CTTTCTTCCCTCATCTCATATTTTCAGGCTAAGTATACATTTTATTCACCAATGCTTTTGTG	540
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Dp	1816	TCTGTGTGTGTGTATAGAGGAGAGGAGCATACCCAGAGACTCCTTGAAGCCCCGGCAG	1875
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BD237936 6169 bp DNA linear PAT 17-JUL-2003
LOCUS Nucleic acids, kits, and methods for the diagnosis, prognosis and
DEFINITION treatment of glaucoma and related disorders.
ACCESSION BD237936
VERSION BD237936.1 GI:33047706
KEYWORDS JP 2002534135-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
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Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
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OS Homo sapiens (human)
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THAI D NGUYEN, JON R POLANSKY, PU CHEN, HUA CHEN PC
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Query Match 81.5%; Score 4888.8; DB 6; Length 6169;
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LOCUS AR242746
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ACCESSION AR242746
VERSION AR242746.1 GI:27289385
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6169)
AUTHORS Nguyen,T.D., Polasky,J.R., Chen,P. and Chen,H.
TITLES Nucleic acids, kits, and methods for the diagnosis, prognosis and
treatment of glioma and related disorders
JOURNAL Patent: US 6475724-A 3 05-NOV-2002;
The Regents of the University of California; Oakland, CA
FEATURES
source
location/Qualifiers
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ORIGIN
Query Match 81.5%; Score 4888.8; DB 6; Length 6169;
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LOCUS AR123663
DEFINITION Sequence 1 from patent US 6171788.
ACCESSION AR123663
VERSION AR123663.1 GI:14109024
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
JOURNAL Patent: US 6171788-A 1 09-JAN-2001;
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ORIGIN

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Qy 181 ACAGGCGACGCGCGCTAATTTTGTATGTTAGTAGAGATGGGTTTACCATATTAG 240
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ACCESSION	BD237934				
VERSION	BD237934.1	GI:33047704			
KEYWORDS	JP 2002534135-A/1.				
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	Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 5300)				
AUTHORS	NGUYEN,T.D., Polansky,J.R., Chen,P. and Chen,H.				
TITLE	Nucleic acid, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders				
JOURNAL	Patent: JP 2002534135-A 1 15-OCT-2002;				
	THE REAGENTS OF THE UNIVERSITY OF CALIFORNIA				
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	PD 15-OCT-2002				
	PF 11-JAN-2000 JP 2000593777				
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	and				
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[illegible]

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ACCESSION	AR242744				
VERSION	AR242744.1	GI:27289383			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				

REFERENCE	1 (bases 1 to 5300)
AUTHORS	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE	Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
JOURNAL	Patent: US 6475724-A 1 05-NOV-2002;
FEATURES	the Regents of the University of California; Oakland, CA
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DB	1276 CGTACGGGTGAGGGTCTGTGTCTTAACCTACCTGATGCTCTACCTGAGTCACTGAC
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QY	181 ACAGGCGCACCCCGGCTAATTTTTTGTATTTGTATGATAGATGGGGTTTCAACATATTAG
DB	1396 ACAGGCGCACCCCGGCTAATTTTTTGTATTTGTATGATAGATGGGGTTTCAACATATTAG
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DB	1456 CCGGCTGCTCTTGAACCTCTGACCTCGAGGATCAACCACTGAGGCTCTTAAAGTGC
QY	301 TGGGATTACAGGCAAGTCAACCGGCGCCGACCAAGGCTCAGTGTTTAATAGAATAAC
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QY	361 TTGAATGGTTTACTTAACCAACAGGGAACAGACAAAGCTGTGATTAATTCAGGAAATTC
DB	1576 TTGAATGGTTTACTTAACCAACAGGGAACAGACAAAGCTGTGATTAATTCAGGAAATTC
QY	421 TTGGGATGGGAAATGTGTGCATGAGCTGCTGCTTAAGTCCAGACACCTGAGCTCATCA
DB	1636 TTGGGATGGGAAATGTGTGCATGAGCTGCTGCTTAAGTCCAGACACCTGAGCTCATCA
QY	481 CTTTCTCCCTCAGCTCTCATTTTTCAGGCTAAGTACATTTTATTCACCATGCTTTGTG
DB	1696 CTTTCTCCCTCAGCTCTCATTTTTCAGGCTAAGTACATTTTATTCACCATGCTTTGTG
QY	541 GTAAAGCTTCAATCGTTACTGAATTAAGATGATACATTAACCTAGTTCATTTGGGACCA
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QY	601 TGTGTGTGTGTATATGGGAGAGAGGCATACCCAGAGACTCTTGAAGCCCCCGGACG
DB	1816 TGTGTGTGTGTATATGGGAGAGAGGCATACCCAGAGACTCTTGAAGCCCCCGGACG
QY	661 AAGTTTCCCTCCAGCTGGGGGAGGCGTGCAGACACCGGGGTCTGGGTGTCTTGAGCA
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DEFINITION	Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders.				
ACCESSION	BD065039				
VERSION	BD065039.1	GI:22610642			
KEYWORDS	JP 2001509669-A/1.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 5299)				
AUTHORS	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.				
TITLE	Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders				
JOURNAL	Patent: JP 2001509669-A 1 24-JUL-2001; THE REGENTS OF THE UNIVERSITY OF CALIFORNIA				
COMMENT	OS Unidentified PN JP 2001509669-A/1 PD 24-JUL-2001 PF 09-JUN-1998 JP 1998532017 PR 28-JUN-1997 US 08/791154,26-SEP-1997 US THAI D NGUYEN, JON R POLANSKY, PU CHEN HUA CHEN PC C12H15/12,C12Q1/68,C07K14/47,A61K31/70 CC Strandedness: Single; CC Topology: Linear; CC Methods for the diagnosis, prognosis and treatment of glaucoma CC treatment of glaucoma and related CC disorders FH Key Location/Qualifiers FT source 1..5300 /organism='unidentified'. FT 1..5299 Location/Qualifiers 1..5299 /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'				
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ORIGIN					
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Best Local Similarity	99.9%; Pred. No. 0;				
Matches 4081; Conservative	0; Mismatches 1; Indels 2; Gaps 1;				
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QY	61 CGTAGAGGTGAGGGTCTGTCTTACACCTACCTGTAAGCTCTACCTGAGCTCACTGC	120			
DB	1276 CGTAGAGGTGAGGGTCTGTCTTACACCTACCTGTAAGCTCTACCTGAGCTCACTGC	1335			
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QY	181 ACAGCGCCACCGCGGCTAATTTTGTATTTGTATAGTAGAATGGAGTTTACACATATTAG	240			
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DB	1516 TGGAGTTACAGGCATGAGTCAACCGCGCCGCGCCAAAGGTCAAGTGTATTAATAGAAATAC	1575			
QY	361 TTGATGTGTTTACTTAAACCAACAGGAAACAGCAAAAGCGTGATATTTTCAAGGATTC	420			
DB	1576 TTGATGTGTTTACTTAAACCAACAGGAAACAGCAAAAGCGTGATATTTTCAAGGATTC	1635			


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Db 1936 ACCGCGAGCCCGTGCCTGCTGCTGTTTGTATCACTCTAGGGAGCCTGTGCTTTCT 1995
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QY	2521	AGGCAATCCCGTTCTCTTTTAAACAGAAAGAAACATTCTTAAGAGTAAAGCCAAACAGAT	2580
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[illegible]

FEATURES
Source

Location/Qualifiers
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ORIGIN

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DB 1336 AACCTCTGCTCCAGGTTCAAGCAATCTCTGTCTAGCTCCGCGTACGCTGAGT 1395
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[illegible]

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LOCUS	BD237935	5304 bp	DNA linear
DEFINITION	Nucleic acids, kits, and methods for the diagnosis, prognosis and		

ACCESSION BD237935
 VERSION BD237935.1 GI:33047705
 KEYWORDS JP 2002534135-A/2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 5304)
 Nguyen T.D., Polansky J.R., Chen P. and Chen H.
 Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
 Patent: JP 2002534135-A 2 15-OCT-2002;
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 OS Homo sapiens (human)
 PN JP 2002534135-A/2
 PD 15-OCT-2002
 PF 11-JAN-2000 JP 2000593777
 PR 11-JAN-1999 US 09/227881, 07-MAY-1999 US 09/306828 PI
 THAI D NGUYEN, JON R POLANSKY, PU CHEN, HUA CHEN PC
 C12N15/09, A61K31/573, A61K45/00, A61P27/06, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC C12N5/10, C12Q1/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
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 CC treatment of glaucoma and related disorders
 FH Key Location/Qualifiers
 FT source 1.5304
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QY 61 CGTAGAGGTGAGGGTCTGTCTTACACCTGATGATGCTTACACCTGAGCTCACTGC 120
 DB 1276 CGTAGAGGTGAGGGTCTGTCTTACACCTGATGATGCTTACACCTGAGCTCACTGC 1335

QY 121 AACCTGCTCCCAAGTCAAGCAATCTCTGCTCAGAGCTCCGCGTGAAGCTGAGACT 180
 DB 1336 AACCTGCTCCCAAGTCAAGCAATCTCTGCTCAGAGCTCCGCGTGAAGCTGAGACT 1395

QY 181 ACAGGCGCACGCCGCGCTAATTTTGTATTGTAAGATGGGGTTTACCAATATTAG 240
 DB 1396 ACAGGCGCACGCCGCGCTAATTTTGTATTGTAAGATGGGGTTTACCAATATTAG 1455

QY 241 CCGGCTGTGCTTGAATCTCTGACCTCAGGTATCAACCACTCAGCTCTCTTAAGTGC 300
 DB 1456 CCGGCTGTGCTTGAATCTCTGACCTCAGGTATCAACCACTCAGCTCTCTTAAGTGC 1515

QY 301 TGGGATTACAGGATAGTCAACGCGCCGCGCAAGAGTCAAGTGTAAATGAAGAAATAC 360
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Db      2836  CATGCTCTTGGGCACTACTACAGCCCTGTGTGACTTTGGCTTATGCAAGCGTCCAA 2895
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ACCESSION	AR242745
VERSION	AR242745.1 GI:27289384
DNA	linear
PAT	20-DEC-2002

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 5304)
TITLE	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H. Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
JOURNAL	Patent: US 6475724-A 2 05-NOV-2002;
FEATURES	The Regents of the University of California; Oakland, CA Location/Qualifiers

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Qy	121	AACCTTGCCCTCCAGGTTCAAGCAATTCCTCTCAGACCTCCCGTAGCTGGACT	180	
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Db	1456	CCCGGCTGCTTTTAACTCCCTGACCTCAGGATGACCAACCTCAGCCCTTAAAGTGC	1515	
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AUTHORS Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and
Polansky,J.R.
TITLE Gene structure and properties of TIGR, an olfactomedin-related
glycoprotein cloned from glucocorticoid-induced trabecular meshwork
cells
JOURNAL J. Biol. Chem. 273 (11), 6341-6350 (1998)
PUBMED 9497363
REFERENCE
AUTHORS Nguyen,T.D., Chen,P., Chen,H. and Polansky,J.R.
TITLE Direct Submision
JOURNAL Submitted (10-JUN-1997) Ophthalmology, University of California San
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Scoring table: IDENTITY NTC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5998.4	99.9	6000	ADJ94187	Adj94187 Human MYO
2	5976.8	99.6	37252	ACN44666	ACN44666 Human gen
3	4888.8	81.5	6169	AAV51368	AAV51368 Human TIG
4	4888.8	81.5	6169	AAAS7486	AAAS7486 A TIGR (c
5	4069.4	67.8	5300	AAAS7484	AAAS7484 A TIGR (c
6	4069.4	67.8	5300	ADFL13152	ADFL13152 Human TIG
7	4069.4	67.8	5300	ADFL13152	ADFL13152 Human tra
8	4068.4	67.8	5300	AAV51361	AAV51361 Human TIG
9	4067.8	67.8	5300	AAV51365	AAV51365 Human TIG
10	4067.8	67.8	5300	AAV51367	AAV51367 Human TIG
11	4067.8	67.8	5300	AAV51363	AAV51363 Human TIG
12	4067.8	67.8	5300	AAV51366	AAV51366 Human TIG
13	4067.8	67.8	5300	AAV51362	AAV51362 Human TIG
14	4065.4	67.6	5304	AAV51364	AAV51364 Human TIG
15	4057.4	66.9	5271	AAAS7485	AAAS7485 A TIGR (c
16	4015.8	46.2	2800	AAAS7511	AAAS7511 A TIGR (c
17	2773.4	46.2	2800	AAZ37968	AAZ37968 Human GLC
18	2773.4	46.2	2800	ADJ99152	ADJ99152 Trabecula
19	2773.4	46.2	2800	ADZ67355	ADZ67355 Human TIG

20	1382.2	23.0	3493	2	AAV37618	AAV37618 Human gla
21	1068.8	17.8	1086	8	ACA64937	ACA64937 Human GLC
22	1068.8	17.8	1086	12	ADQ18110	ADQ18110 Human sof
23	681.4	11.4	2117	8	ABZ58478	ABZ58478 Human myo
24	681.4	11.4	2117	8	ABX10137	ABX10137 Human cdn
25	677.8	11.3	2145	4	AAAS15366	AAAS15366 CDNA enco
26	668.4	11.1	2082	11	ACN44667	ACN44667 Human mfn
27	664.4	11.1	2115	12	ADQ22683	ADQ22683 Human sof
28	641.4	10.7	2031	4	ADQ8141	ADQ8141 Human tra
29	640.4	10.7	1548	2	AAV51391	AAV51391 Human TIG
30	640.4	10.7	1548	3	AAAS7509	AAAS7509 CDNA enco
31	640.4	10.7	1890	2	AAAS7606	AAAS7606 Human TIG
32	640.4	10.7	1999	2	AAV08904	AAV08904 TIGR prot
33	640.4	10.7	1999	2	AAV81910	AAV81910 Human tra
34	640.4	10.7	1999	5	AAAS7528	AAAS7528 Human TIG
35	640.4	10.7	2000	2	AAV33484	AAV33484 Trabecula
36	626.4	10.4	2061	9	ACH03575	ACH03575 CDNA enco
37	618	10.3	30057	11	ACN44664	ACN44664 Mouse gen
38	608	10.1	2800	3	AAZ37971	AAZ37971 Mouse GLC
39	604.4	10.1	1512	2	AAV08905	AAV08905 TIGR prot
40	604.4	10.1	1512	5	AAAS7529	AAAS7529 Human TIG
41	604.4	10.1	1515	3	AAZ37974	AAZ37974 Human GLC
42	604.4	10.1	1515	8	ABX10138	ABX10138 Human TIG
43	604	10.1	604	12	ACH91949	ACH91949 Human gen
44	603.4	10.1	1512	2	AAV37619	AAV37619 Human gla
45	556.6	9.3	1969	2	AAZ30152	AAZ30152 Trabecula

ALIGNMENTS

RESULT 1

ADJ94187
ADJ94187 strand: DNA, 6000 BP.

ADJ94187;

06-MAY-2004 (first entry)

Human MYOC gene in which glaucoma-inducing mutations are detected.

ds; glaucoma; detection; mutation; MYOC.

Homo sapiens.

WO2003083108-A1.

09-OCT-2003.

19-MAR-2003; 2003WO-JP003307.

29-MAR-2002; 2002JP-00093443.

(SYSM-) SYSMEX CORP.

Asano K, Takahata T, Numada S, Masago A, Kouchi Y;

WPI; 2003-804059/75.

Examining genes to assess the risk of the onset of glaucoma by detecting mutations in the MYOC gene or the region upstream from it.

Claim 3; SEQ ID NO 1; 42pp; Japanese.

The invention relates to a method of examining genes to assess the risk of the onset of glaucoma comprising detection of at least two mutations in the glaucoma related gene encoding region and/or a region upstream from it. The glaucoma related gene is preferably the MYOC gene. The method is useful for the prevention or early detection of glaucoma. This sequence corresponds to the MYOC gene in which mutations are detected.

Sequence 6000 BP; 1586 A; 1285 C; 1499 G; 1630 T; 0 U; 0 Other;

Query Match 99.9%; Score 5998.4; DB 10; Length 6000;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 5999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCTCCACAGGAAGTCTCCCACTGACCTTGTGATACAGATGTTACAGCCAGAAAGTTC
DB 1 GCTCCACAGGAAGTCTCCCACTGACCTTGTGATACAGATGTTACAGCCAGAAAGTTC
QY 61 CGTAGAGGTGAGGGCTGTGTCTTACACCTACCTATGCTCTACACCTGAGCTCACTGC
DB 61 CGTAGAGGTGAGGGCTGTGTCTTACACCTACCTATGCTCTACACCTGAGCTCACTGC
QY 121 AACCTGCTCCCAAGGTTCAAGCAATTCTCTGTCTCAGCCTCCCGGTAGCTGGAAT
DB 121 AACCTGCTCCCAAGGTTCAAGCAATTCTCTGTCTCAGCCTCCCGGTAGCTGGAAT
QY 181 ACAGGCGCACGCCCGCTAAATTTTGTATTTGTATGTAGATGAGATGGGGTTTCAACATATTAG
DB 181 ACAGGCGCACGCCCGCTAAATTTTGTATTTGTATGTAGATGAGATGGGGTTTCAACATATTAG
QY 241 CCCGCTGCTGTGAACCTCTGACCTGAGGTATCCACCCACCTGAGCCTCTAAAGTTC
DB 241 CCCGCTGCTGTGAACCTCTGACCTGAGGTATCCACCCACCTGAGCCTCTAAAGTTC
QY 301 TGGGATTAACAGCATGATGTCACCGCGCCCGGCAAGGTCAGTGTATTAAGAAATAC
DB 301 TGGGATTAACAGCATGATGTCACCGCGCCCGGCAAGGTCAGTGTATTAAGAAATAC
QY 361 TTGAATGCTTTAATAACCAAGGAAACAGACAAAAGCTGTGATTAATTTCAAGGATTC
DB 361 TTGAATGCTTTAATAACCAAGGAAACAGACAAAAGCTGTGATTAATTTCAAGGATTC
QY 421 TTGGGATGGGGAATGTGTCATGAGCTGCTGCTGATCCAGACCACTGGGCTCATCA
DB 421 TTGGGATGGGGAATGTGTCATGAGCTGCTGCTGATCCAGACCACTGGGCTCATCA
QY 481 CTTTCTTCCTCATCTCTCAATTTTCAAGGTCAGTATCAATTTTATTCACCATGCTTTTGTG
DB 481 CTTTCTTCCTCATCTCTCAATTTTCAAGGTCAGTATCAATTTTATTCACCATGCTTTTGTG
QY 541 GTTAACCTTCACATGTTACTGAATAATAGAGTATCATTAACCTAGTTTCAATTTGGGGCA
DB 541 GTTAACCTTCACATGTTACTGAATAATAGAGTATCATTAACCTAGTTTCAATTTGGGGCA
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DB 601 TCTGTGTGTGTATAGGGGAGAGGAGCATACCCAGAGACTCTTGAAGCCCGGAG
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DB 841 TCTGCGACAGCACAGAGCAAAATGATGAGCAAGCAAGTCACTGCTTACTCTGTGAG
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DB 1321 TGAAGGGGTGCTGAAGAGCAGAAAGTGAAGAGGCAAGGCTGAAGCTGCCAGATGTC
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QY 1921 AAGAGGAGAGCTGAGAGCACTGAGCAAGGGAGGTGAGAGGGGAGCAGAGAGGCA
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Db 3781 GT 3840
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Qy 4141 TGCTGAGCTTTGGGCTGAGATGCGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4200
Db 4141 TGCTGAGCTTTGGGCTGAGATGCGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4200
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Db 4501 CGGAGCACTGAGAAACCAAAACAGAGAGTTGAGAGCTGCTACAGCAACCTCTCCGA 4560
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Db 4561 GACAAATCAGTTCTTGAGAGAGAGAGAGAGCGACTTAAGGCAAGAAATGAGATCTGGCC 4620
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Db 5041 CCTTTTGAAGAACTATCCTTTTGAACCTTTGTCTCAGATTGTATTGTACTCTTTTGA 5100
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Db 5101 TGTTAATATGACCTTATTTATGAATTAATGATTTGGGAATGATTAATAGTGTGA 5160
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Db 5341 CTGGTCCCTTCTTGGCTTAAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5400
Oy 5401 TGTGGGGAGAGTCTTCTTAATAGCTGGAGAGATGATTTGTGTCTTTTGTGAAG 5460
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    |||
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Oy 5581 AAAAAGGGGTGGGAGAGGCTTGTCTTAATTAATTAAGAGACTAAAGAAATGTGTAAACCA 5640
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Oy 5641 ATGTAAGTCAATGACTTGTGATTGTTGCTTCAATCAAGGGGGAGAGAGAGAGAGAGAGAG 5700
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Db 5641 ATGTAAGTCAATGACTTGTGATTGTTGCTTCAATCAAGGGGGAGAGAGAGAGAGAGAGAG 5700
Oy 5701 AGTTTGGGATTAATCTGAGGCAATTTGACTGCTCAATTAATGTTACTGTATTAATGTTCA 5760
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Oy 5761 GTTTCTGTGAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 5820
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Oy 5821 TACATGCTTAAGTACCCAGGGGTGAGGCGTCAAGATGTCTGCAATTTGCTCAATGGTT 5880
    |||
Db 5821 TACATGCTTAAGTACCCAGGGGTGAGGCGTCAAGATGTCTGCAATTTGCTCAATGGTT 5880
Oy 5881 GAAGAAAGACTGCAATATATATATATATATATATATATATATATATATATATATATATAT 5940
    |||
Db 5881 GAAGAAAGACTGCAATATATATATATATATATATATATATATATATATATATATATATAT 5940
Oy 5941 ATATTAACTGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6000
    |||
Db 5941 ATATTAACTGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6000

```

RESULT 2

ACN44666
ID ACN44666 standard; DNA; 37252 BP.

AC ACN44666;

DT 18-NOV-2004 (first entry)

DE Human genomic sequence hCG37091.

KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

OS Homo sapiens.

PN WO2003073826-A2.

PD 12-SEP-2003.

PF 28-FEB-2003; 2003WO-US006235.

PR 01-MAR-2002; 2002US-00087192.

PA (SAGR-) SAGRES DISCOVERY.

PI Morris DW;

DR MPI; 2003-328604/31.

PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
comprises a nucleotide sequence.

PS Claim 1; SEQ ID NO 1228; Opp; English.

CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinosmas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoa Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoa Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
US2002182586A1, for which no sequence data was published
CX

SQ Sequence 37252 BP; 10006 A; 8724 C; 8201 G; 10321 T; 0 U; 0 Other;

Query Match	99.6%	Score 5976.8	DB 11	Length 37252
Best Local Similarity	99.6%	Score 5976.8	DB 11	Length 37252

best local similarity 99.96; P-rod. NO. 0;
 Matches 5993; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY	1	GCTCACAAGGAAGTGTCCCACTCAGACCTTCTGCATACAGATGTTACAGCCAGAAAGCTC	60
Dp	5946	GCTCACAAGGAAGTGTCCCACTCAGACCTTCTGCATACAGATGTTACAGCCAGAAAGCTC	6005
QY	61	CGTAGAGGTAGAGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGC	120
Dp	6006	CGTAGAGGTAGAGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGC	6065
QY	121	AACCTCTGCTCCAGAGTTCAAGCAATTCTCTGTCTCAGCTCTCCGGTAGCTGGAGCT	180
Dp	6066	AACCTCTGCTCCAGAGTTCAAGCAATTCTCTGTCTCAGCTCTCCGGTAGCTGGAGCT	6122
QY	181	ACAGGCGCAGCCCGGCTAATTTTTGTATGTGTATGATTAAGATGGGGTTCAACATATTAG	240
Dp	6126	ACAGGCGCAGCCCGGCTAATTTTTGTATGTGTATGATTAAGATGGGGTTCAACATATTAG	6185
QY	241	CCCGGCTGCTGTGAACTCTGAGCTCAGTGTATCACCCACTCAGCCTCCTAAAGTGC	300
Dp	6186	CCCGGCTGCTGTGAACTCTGAGCTCAGTGTATCACCCACTCAGCCTCCTAAAGTGC	6245
QY	301	TGGGATTCAGGCAATGAGTCAACCGGCGCCGACAAAGGCTCAGTGTATTAAGAAATAAC	360
Dp	6246	TGGGATTCAGGCAATGAGTCAACCGGCGCCGACAAAGGCTCAGTGTATTAAGAAATAAC	6305
QY	361	TTGAATGGTTTACTTAACCAACAGGGAAACAGACAAAGCTGTATATTTCAGGGATTTC	420
Dp	6306	TTGAATGGTTTACTTAACCAACAGGGAAACAGACAAAGCTGTATATTTCAGGGATTTC	6365
QY	421	TTGGGATGGGGAATGATGTCATAGAGCTCTGCTGACCTGACCCAGACCATGTGGCTCATCA	480
Dp	6366	TTGGGATGGGGAATGATGTCATAGAGCTCTGCTGACCTGACCCAGACCATGTGGCTCATCA	6425
QY	481	CTTTCCTTCCTCATCTCTCATTTTTCAGGCTAAGTTACCAATTTATTCACCAATGCTTTGTG	540
Dp	6426	CTTTCCTTCCTCATCTCTCATTTTTCAGGCTAAGTTACCAATTTATTCACCAATGCTTTGTG	6485
QY	541	GTAGAGCTCCACATGCTTACTGAAATTAAGATTAATACATTAACCTAGTTTCATTTGGGCGCA	600
Dp	6486	GTAGAGCTCCACATGCTTACTGAAATTAAGATTAATACATTAACCTAGTTTCATTTGGGCGCA	6545
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Dp	6546	TCTGTGTGTGTGTATAGGGGAGAGAGGCACTACCCAGACATCTCTGTAAAGCCCCCGGAG	6605
QY	661	AGGTTTCTCTTCAGCTGGGGGAGCCTTCAGACACCCGGGGTCTGGGTGTCTTGAGCA	720
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QY	721	ACCGGCAAGCCCGGCACTGGTGTGTTTGTATTAACCTCTTAAGGACTGTGTCTTCT	780
Dp	6666	ACCGGCAAGCCCGGCACTGGTGTGTTTGTATTAACCTCTTAAGGACTGTGTCTTCTTCT	6725

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Db	6846	GTGACAGTTTCTCATGTGAAGCGTGCAGAAAGAAATTATATGCGACCACTTAAACCCA	6905
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QY	1201	AGAGGAAACCTAGTCTTAACGAGAAATCTGAGAGGGGACAGTGTTTCTCCAGAGGAAAGG	1260
Db	7146	AGAGGAAACCTAGTCTTAACGAGAAATCTGAGAGGGGACAGTGTTTCTCCAGAGGAAAGG	7205
QY	1261	GCTTCCACGTCCAGAGAAATTCAGAGAGTGTTGGGAGCTGCAGGAGTGGGGACCTGTGGGC	1320
Db	7206	GCTTCCACGTCCAGAGAAATTCAGAGAGTGTTGGGAGCTGCAGGAGTGGGGACCTGTGGGC	7265
QY	1321	TGACCGGAGTGTCTGAAGAGGCGAGAAAGTGTAAAGGGCGAGCTGAGCTGCCAGATGTTCT	1380
Db	7266	TGACCGGAGTGTCTGAAGAGGCGAGAAAGTGTAAAGGGCGAGCTGAGCTGCCAGATGTTCT	7325
QY	1381	AGTGTGTGTCACGGGGCTGGAGAGTTTTCGTTGCTCTGTGAGGCTTTTATCTTTTCT	1440
Db	7326	AGTGTGTGTCACGGGGCTGGAGAGTTTTCGTTGCTCTGTGAGGCTTTTATCTTTTCT	7385
QY	1441	CTGCTTGAGAGAGAAAGTCTATTTTCATGAAAGGATGAGATTTCTAAAGTCAGCTGTT	1500
Db	7386	CTGCTTGAGAGAGAAAGTCTATTTTCATGAAAGGATGAGATTTCTAAAGTCAGCTGTT	7445
QY	1501	AAAAATCCAGGGTGTGATGGGTTTTCTTCACGAAGGCCCTTATTTAATGGAATATAG	1560
Db	7446	AAAAATCCAGGGTGTGATGGGTTTTCTTCACGAAGGCCCTTATTTAATGGAATATAG	7505
QY	1561	GAACCGAGCTCATTTCTTAGCCGTTAATTCACAGGAAGAGTACCTGAGTCTTTTCTTT	1620
Db	7506	GAACCGAGCTCATTTCTTAGCCGTTAATTCACAGGAAGAGTACCTGAGTCTTTTCTTT	7565
QY	1621	CATGCTCTTGAGGCAACTACAGCCCTGTGATGTCCTGTGAGGAGGAGATGTTGAGAGGGG	1680
Db	7566	CATGCTCTTGAGGCAACTACAGCCCTGTGATGTCCTGTGAGGAGGAGATGTTGAGAGGGG	7625
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Db	7626	AACCTTGAATCAGAGACTCGGTTTTCTTTCTGATCTGCAATGGTGTGGCTGTGCGAC	7685
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Db	7686	CGGGGCAATGTCTCTCTCCCTCCCTGGGCAATAGTCTTCTGTGCTAATAAGCCTTGTGA	7745
QY	1801	GCTCTCGTGTCTGTGAACAATCCCTGTGATTTCTGTGAGGGGAGATGTTGAGAGGGG	1860
Db	7746	GCTCTCGTGTCTGTGAACAATCCCTGTGATTTCTGTGAGGGGAGATGTTGAGAGGGG	7805
QY	1861	AAGAGGACAGACTGTGAGCAGCTGACCCAAGGGAGGTGAGGGGGGACAGAGACGAG	1920

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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT exon 5301..5940
XX FT CDS /*tag= a
FT /*number= 1
FT /*tag= b
FT /*product= "TIGR"
FT /*note= "partial coding sequence"
FT /*tag= c
FT /*number= 1
FT /*note= "partial intron sequence"
XX PN W09832850-A1.
XX PD 30-JUL-1998.
XX PR 09-JAN-1998; 98MO-US000468.
XX PR 28-JAN-1997; 97US-00791154.
XX PR 26-SEP-1997; 97US-00938669.
XX PA (RSCC ) UNIV CALIFORNIA.
XX PI Nguyen TD, Polansky JR, Chen P, Chen H;
XX WP1; 1998-427946/36.
XX Use of TIGR nucleic acid sequences - used for, e.g. developing products
XX for diagnosis, prognosis and treatment of glaucoma.
XX Claim 37; Fig 3; 105pp; English.
XX This sequence is a trabecular meshwork induced glucocorticoid response
XX protein (TIGR) upstream region and exon 1. This DNA sequence can be used
XX in a method for diagnosing glaucoma in a patient. The method involves the
XX detection of polymorphisms whose presence is predictive of a mutation
XX affecting TIGR response in the patient and can be diagnostic of glaucoma
XX or steroid sensitivity. Base substitutions and base additions upstream of
XX and within TIGR exons can also be used to diagnose glaucoma
XX
SQ Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 U; 0 Other;
Query Match 81.5%; Score 4888.8; DB 2; Length 6169;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;
QY 1 GGTCCAGGAAAGTCTCCCACTCTGAGCTTGTGATCAGATCAGATGTTACAGCCAGAAAGCTC 60
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QY 61 CGTGAAGGTGAGGCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTCACTGC 120
DB 1276 CGTGAAGGTGAGGCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTCACTGC 1335
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DB 1336 AACCTGTGCTCCCAAGTTCAGCAATTTCTCTGTCTCAGCTCCCGGTAGCTGGACT 1395
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DB 2356 AATGCTGTGTGATCTGAGCTGAGACTCTCTTGCTCCAGGCTCCAGAAAGAAATAG 2415
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QY 1441 CTGCTTGAAGAGAGAGTCTATTTTCATGAAGAGATGCACTTTTCATTAAGTCAGCTGTT 1500
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 Db 2656 CTGCTTGAAGAGAGAGAGTCTATTTTCATGAAGAGATGCACTTTTCATTAAGTCAGCTGTT 2715
 |||||
 QY 1501 AAAATTCAGGGGTGTCATGGGTTTTCTTCAGGAAGGCTTTATTTAATGGGAATATAG 1560
 |||||
 Db 2716 AAAATTCAGGGGTGTCATGGGTTTTCTTCAGGAAGGCTTTATTTAATGGGAATATAG 2775
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 QY 1561 GAAGCAGCTCATTTTCTAGGCGGTTAATTCACGGAAGAAGTACGTGAGTCTTTCTTT 1620
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 Db 2776 GAAGCAGCTCATTTTCTAGGCGGTTAATTCACGGAAGAAGTACGTGAGTCTTTCTTT 2835
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 QY 1621 CATGCTTCTGAGCAACTACAGCCCTGTGTGAATTGGCTTATGCAAGCGTGCAG 1680
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 Db 4755 CGGCTTCTATAGGAATGCTCCCTGGAGCTGTAGAGGAGTGTCTGTGCTTGGCT 4814
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 QY 3600 GGTGTATTTTCTGTGCTCCCTGCTACGTTTAAAGACTTGTGGATCTCCAGTTCC 3659
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[illegible]

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Db	5955	TGGGGGGGACTCTGATGTTTCAGAGGTGATGATGAGTCTGATGAGTCTGCTTACAGAGGAGCTCCA	6014		
Qy	4798	GGGCTCCCTGCTGAGCCCTTTCTCTAGAGACTGACAGAGTACAGACAGATGAAATTA	4857		
Db	6015	GGCTCC-----CCTGCCCTTTCTCTTAGAGACTGACAGAGTACAGACAGATGAAATTA	6070		
Qy	4858	AGGAAGCAGACGCGATCACTTCAAGATTACTAGTAATTTAGCTCTGAGAGCTTCATT	4917		
Db	6071	AGGAAGCACA--CGATCACTTCAAGATTACTAGTAATTTAGCTCTGAGAGCTTCATT	6129		
Qy	4918	TAGATTAGTGTTCAGAGTCTTTGTGCCCTCCATGTCAG	4957		
Db	6130	TAGATTAGTGTTCAGAGTCTTTGTGCCCTCCATGTCAG	6169		
RESULT 4					
AAAS7486					
ID	AAAS7486	standard; DNA; 6169 BP.			
XX	AAAS7486;				
XX	20-OCT-2000	(first entry)			
DT					
XX	A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.				
XX					
XX	TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;				
KW	glaucoma; steroid sensitivity; progressive ocular hypertension;				
KW	vision loss; ss.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	mutation	replace(4256, G)			
FT		/*tag= d			
FT		/note= "TIGRmt4 mutant"			
FT	mutation	replace(4337, G)			
FT		/*tag= a			
FT		/note= "TIGRmt1 mutant"			
FT	mutation	replace(4950, T)			
FT		/*tag= b			
FT		/note= "TIGRmt2 mutant"			
FT	mutation	4998			
FT		/*tag= c			
FT		/note= "GTGT added to produce TIGRmt3 mutant"			
FT	mutation	replace(5113, C)			
FT		/*tag= e			
FT		/note= "TIGRmt11 mutant"			
XX					
PN	WO200042220-A1.				
XX					
XX	20-JUL-2000.				
XX					
PF	11-JAN-2000; 2000WO-US000559.				
XX					
PR	11-JAN-1999; 99US-00227881.				
PR	07-MAY-1999; 99US-00306828.				
XX					
PA	(REGC) UNIV CALIFORNIA.				
XX					
PI	Nguyen TD, Polansky JR, Chen P, Chen H;				
XX					
XX	WPI; 2000-491060/43.				
XX					
PT	Diagnosis, prognosis and treatment of glaucoma, based on detecting				
PT	specific polymorphisms in the promoter of the trabecular meshwork				
PT	inducible glucocorticoid receptor gene.				
XX					
PS	Claim 37, Page 105-107; 122pp; English.				
CC	The present sequence represents a TIGR (trabecular meshwork inducible				

CC glucocorticoid receptor) promoter. The specification describes a method
 CC for the diagnosis, prognosis and treatment of glaucoma, based on
 CC detecting specific polymorphisms in the promoter of the TIGR gene. The
 CC method is used for diagnosis and prognosis of glaucoma (of all types),
 CC steroid sensitivity and progressive ocular hypertension (that leads to
 CC loss of vision. Glaucoma can be treated by administering an agent that
 CC binds to cis-acting elements within the TIGR promoter. The TIGR promoter
 CC (or other regulatory regions) can be used to express homologous or
 CC heterologous genes, particularly for tissue-specific expression of
 CC therapeutic transgenes for treating glaucoma, also to generate transgenic
 CC animals and in screening for compounds (specific modulators) with
 CC diagnostic or therapeutic potential. Fragments of the TIGR sequence can
 CC be used as amplification primers or probes, e.g. for isolating related
 CC sequences in non-human animals
 XX

Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 U; 0 Other;

Query Match 81.5%; Score 4888.8; DB 3; Length 6169;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;

QY 1 GCTCCACAGGAAGTCTCCACCTCTAGACTTTCGATCAGATGTTACAGCCAGAAAGCTC 60
 DB 1216 GCTCCACAGGAAGTCTCCACCTCTAGACTTTCGATCAGATGTTACAGCCAGAAAGCTC 1275
 QY 61 CGTAGAGGTGAGGGTCTGTGTCTTACACCTATGCTTACACCTGAGCTACCTG 120
 DB 1276 CGTAGAGGTGAGGGTCTGTGTCTTACACCTATGCTTACACCTGAGCTACCTG 1335
 QY 121 AACCTGTGCTCCAGAGTTCAAGCAATTCCTGTCTCAGCCCTCCGCGTAGTGGAGCT 180
 DB 1336 AACCTGTGCTCCAGAGTTCAAGCAATTCCTGTCTCAGCCCTCCGCGTAGTGGAGCT 1395
 QY 181 AACAGGGACGCGCGGCTAATTTTGTATTTGTAAGATGGGTTTACCATATTAAG 240
 DB 1396 AACAGGGACGCGCGGCTAATTTTGTATTTGTAAGATGGGTTTACCATATTAAG 1455
 QY 241 CCGCGGTGCTTGAATCTCCAGCTCAGGTGATCCACCCCTCAGCCCTCTTAAAGTG 300
 DB 1456 CCGCGGTGCTTGAATCTCCAGCTCAGGTGATCCACCCCTCAGCCCTCTTAAAGTG 1515
 QY 301 TGGGATTAAGAGCATGATGACCGCGCGCGGCAAGGGTCACTGTTTAAATGAAGAAATAC 360
 DB 1516 TGGGATTAAGAGCATGATGACCGCGCGCGGCAAGGGTCACTGTTTAAATGAAGAAATAC 1575
 QY 361 TTGAATGTTTACTAAACCAACAGGGAACAGCAAAAGCTGATTAATTTACAGGATTC 420
 DB 1576 TTGAATGTTTACTAAACCAACAGGGAACAGCAAAAGCTGATTAATTTACAGGATTC 1635
 QY 421 TTGGGATGGGGAATGGTGCCATGAGCTGCTGCTAGTCCAGACCACTGTCCTATCA 480
 DB 1636 TTGGGATGGGGAATGGTGCCATGAGCTGCTGCTAGTCCAGACCACTGTCCTATCA 1695
 QY 481 GTTCTTCTCCCTCACTCTCAATTTTCAGGCTAAGTTACATTTTATTCACCATGCTTTGTG 540
 DB 1696 GTTCTTCTCCCTCACTCTCAATTTTCAGGCTAAGTTACATTTTATTCACCATGCTTTGTG 1755
 QY 541 GTTAAGCTTCACATCGTTACTGAATTAAGATTAATTAATTAATTAATTAATTAATTAATTA 600
 DB 1756 GTTAAGCTTCACATCGTTACTGAATTAAGATTAATTAATTAATTAATTAATTAATTAATTA 1815
 QY 601 TCTGTGTGTGTGTATATGAGGAGAGGAGGATACCCCAAGACCTCTTGAAGCCCGGAG 660
 DB 1816 TCTGTGTGTGTGTATATGAGGAGAGGAGGATACCCCAAGACCTCTTGAAGCCCGGAG 1875
 QY 661 AAGTTTCTCTCTCAAGCTGGGAGAGCCCTGCAAGCAACCCGCGGTCTCTGAGTCTTGAAGA 720
 DB 1876 AAGTTTCTCTCTCAAGCTGGGAGAGCCCTGCAAGCAACCCGCGGTCTCTGAGTCTTGAAGA 1935
 QY 721 AACTGCAAGCCGATGCACTGATGTTTGTATATCACTCTTAAGGAACTGTGCTTTCT 780
 DB 1936 AACTGCAAGCCGATGCACTGATGTTTGTATATCACTCTTAAGGAACTGTGCTTTCT 1995

QY 781 ATTCTGTGTGACTCGTTATTCATCATCAGGACATTCATGACAAATTAATGAGTACTTATA 840
 DB 1996 ATTCTGTGTGACTCGTTATTCATCATCAGGACATTCATGACAAATTAATGAGTACTTATA 2055
 QY 841 TCTGCAGACACCAAGACAAAATGTTGAGCAAAAGCATCTGCCCTTACCTTGTGAG 900
 DB 2056 TCTGCAGACACCAAGACAAAATGTTGAGCAAAAGCATCTGCCCTTACCTTGTGAG 2115
 QY 901 GTGACAGTTTCTCATGAGGAAGCTGTGCAAGAAATTAATTAATGACCACTTAAACCA 960
 DB 2116 GTGACAGTTTCTCATGAGGAAGCTGTGCAAGAAATTAATTAATGACCACTTAAACCA 2175
 QY 961 GTGCTAAAGAAAGAAATTAACACCATCTTGAAGATTTGTGAGCAATCCCTTAACA 1020
 DB 2176 GTGCTAAAGAAAGAAATTAACACCATCTTGAAGATTTGTGAGCAATCCCTTAACA 2235
 QY 1021 GGGCACTTCCCTAGCGCCCCCTGCTGCTCATCTGTGCCGAGAGGCCCAAGCCGAGT 1080
 DB 2236 GGGCACTTCCCTAGCGCCCCCTGCTGCTCATCTGTGCCGAGAGGCCCAAGCCGAGT 2295
 QY 1081 CTTCAGAGCTCTCTCTCATATGTCACAGCGCTGACGCTGCGCTGCTCCGCTG 1140
 DB 2296 CTTCAGAGCTCTCTCTCATATGTCACAGCGCTGACGCTGCGCTGCTCCGCTG 2355
 QY 1141 AATCGTCTGTGATCTGAGGTGAGACTCTTGTGCTCAGGCTCCAGAAAGAAATAG 1200
 DB 2356 AATCGTCTGTGATCTGAGGTGAGACTCTTGTGCTCAGGCTCCAGAAAGAAATAG 2415
 QY 1201 AAGAGGAAATCTAGTCTAACGAGAAATCTGGAAGGGAACAGTGTTCCTCAGAGGAAAGG 1260
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 QY 1261 GCTCTCAGCTCCAGAGAAATTCAGAGGTGGGACCTGCAAGGAGTGGGACGCTGGGCT 1320
 DB 2476 GCTCTCAGCTCCAGAGAAATTCAGAGGTGGGACCTGCAAGGAGTGGGACGCTGGGCT 2535
 QY 1321 TGAGCGGGGTGTAAGAGGAGGAGTGAAGAGGCAAGGCTGAGCTGCCAGATGTC 1380
 DB 2536 TGAGCGGGGTGTAAGAGGAGGAGTGAAGAGGCAAGGCTGAGCTGCCAGATGTC 2595
 QY 1381 AGTGTGTTTCAAGGGGCTGGGAGTTCGTTCTCTCTGAGGCTTTTATCTTTTCT 1440
 DB 2596 AGTGTGTTTCAAGGGGCTGGGAGTTCGTTCTCTCTGAGGCTTTTATCTTTTCT 2655
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 DB 2656 CTGCTTGAAGAGAAAGTCTATTTCAATGAAGGATGCAATTTATTAAGTCACTGTT 2715
 QY 1501 AAAATTCAAGGATGTCATGAGGTTTCTCTCAAGAGGCTTTTAAATGGGAATTAAG 1560
 DB 2716 AAAATTCAAGGATGTCATGAGGTTTCTCTCAAGAGGCTTTTAAATGGGAATTAAG 2775
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 QY 1621 CATGCTTCTGGGCACTACTCAAGCTGTGTGAGCTTGTGCTTATGCAAGCGTCA 1680
 DB 2836 CATGCTTCTGGGCACTACTCAAGCTGTGTGAGCTTGTGCTTATGCAAGCGTCA 2895
 QY 1681 AACCTTGAATCAAGAGACTGCTGTTTCTTGTGTTCTGCAATGTTGTGTGCAAC 1740
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 QY 1801 GCTCTGCTTCTGTGAACAATTCCTGTGATTTCTGTGAGGGGGAATGTTGAGAGGG 1860
 DB 3016 GCTCTGCTTCTGTGAACAATTCCTGTGATTTCTGTGAGGGGGAATGTTGAGAGGG 3075
 QY 1861 AAGAGGAGAGCTGAGCACTGATGACAGGGGAGTGAAGGGGGAACAGAAAGGACAG 1920

Db	3076	AAGAGGCAAGCTGGAGCAGCTAGCCACAGGGGAGGTGAGGGGACAGGAGGCAAGG	3135
Qy	1921	CAGAAAGCTGGGTGCTCCATCAGTCCCTGACCTGATCAAGCTCCAGACCCGAGGCCA	1980
Db	3136	CAGAAAGCTGGGTGCTCCATCAGCTCTCACTGATACGCTCAAGACTCCAGAGCCGAGGCCA	3195
Qy	1981	CAATGCTTCAGGAAAGCTCAATATGAAACCCACAGCCACATTTTCTTCCCTTAAGCATAGAC	2040
Db	3196	CAATGCTTCAGGAAAGCTCAATATGAAACCCACAGCCACATTTTCTTCCCTTAAGCATAGAC	3255
Qy	2041	AATGGCATTTGGCAATTAACCAAAAAGAAATGACAGAGCACTAAGCTGGTGGATGCTTTGGCTG	2100
Db	3256	AATGGCATTTGGCAATTAACCAAAAAGAAATGACAGAGCACTAAGCTGGTGGATGCTTTGGCTG	3315
Qy	2101	GCATTCAAAAACCTGGGCGACAGACAAAGTGGAAAAATGCGAGAGATTTGTTAACTTTTCAACC	2160
Db	3316	GCATTCAAAAACCTGGGCGACAGACAAAGTGGAAAAATGCGAGAGATTTGTTAACTTTTCAACC	3375
Qy	2161	TGACCAAGACCCACGACGAGCTCAGCAGTGAAGCTGTCACAGCACGAGATGACCTTGACGCGC	2220
Db	3376	TGACCAAGACCCACGACGAGCTCAGCAGTGAAGCTGTCACAGCACGAGATGACCTTGACGCGC	3435
Qy	2221	AGGGAGAGAGAAAGAAAAGAGAGGATAGTGTATAGACAAAGAAACAGATTTCACTTCAAG	2280
Db	3436	AGGGAGAGAGAAAGAAAAGAGAGGATAGTGTATAGACAAAGAAACAGATTTCACTTCAAG	3495
Qy	2281	GGCATGAGGAATTTGACACAGAGGATTAATAGTCCACGATGATCTGGGTTCTAGAGGACAGG	2340
Db	3496	GGCATGAGGAATTTGACACAGAGGATTAATAGTCCACGATGATCTGGGTTCTAGAGGACAGG	3555
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Qy	2521	AGGGCAATCCCGTTTCTTTTAAACAGAAAGAAAACCTCTTAAGATAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCCGTTTCTTTTAAACAGAAAGAAAACCTCTTAAGATAAGCCAAACAGAT	3795
Qy	2581	TCAAGCTTAGGCTTGTGCTGACCTATATGATGGTTTTTGAAGAAATCATTTCAAGGATGTT	2640
Db	3796	TCAAGCTTAGGCTTGTGCTGACCTATATGATGGTTTTTGAAGAAATCATTTCAAGGATGTT	3855
Qy	2641	TACTATCTGATTCAGAAAAATGACCTAAGAACCTTTGGTCAGCTGTAAACAAACCCCAT	2700
Db	3856	TACTATCTGATTCAGAAAAATGACCTAAGAACCTTTGGTCAGCTGTAAACAAACCCCAT	3915
Qy	2701	TTGTAAATGTCTCAAGTTCAGGCTTAACCTGACAGAACCAATCAATATAGATAGATCTTT	2760
Db	3916	TTGTAAATGTCTCAAGTTCAGGCTTAACCTGACAGAACCAATCAATATAGATAGATCTTT	3974
Qy	2761	AGAGCAAACTGTGTTTCTCCAC-TCTGAGGTGAGTCTGCCAGGGCAGTTTGAAGATATTT	2819
Db	3975	AGAGCAAACTGTGTTTCTCCAC-TCTGAGGTGAGTCTGCCAGGGCAGTTTGAAGATATTT	4034
Qy	2820	TACTTCACAAAGATTGACACGTGTGTGGTATTAAACAATATTAATGCTCAAGGCAAT	2879
Db	4035	TACTTCACAAAGATTGACACGTGTGTGGTATTAAACAATATTAATGCTCAAGGCAAT	4094
Qy	2880	CATTATTCAAGTGGCTTAAGATTAATTTCTGACAGTTTGGTATATTTATTGGCTATTC	2939
Db	4095	CATTATTCAAGTGGCTTAAGATTAATTTCTGACAGTTTGGTATATTTATTGGCTATTC	4154
Qy	2940	CATTTCCTTTTGTTTTTTCTCTTGGATTATATATGTAAGCAGGATTTATTAACCTA	2999

[illegible]

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QY 4078 CACAGCAGAGCTTTCAGAGAAAGCTCACCAAGCTCTGCAATGAGTTCTTCTGCA 4137
DB 5295 CACAGCAGAGCTTTCAGAGAAAGCTCACCAAGCTCTGCAATGAGTTCTTCTGCA 5354
QY 4138 CATTGTCGACGCTTTGGGCTGAGATGCCAGCTGCTGCTGCTTGGGCTGCTG 4197
DB 5355 CATTGTCGACGCTTTGGGCTGAGATGCCAGCTGCTGCTGCTTGGGCTGCTG 5414
QY 4198 GTGTGGGATGTGGGGGCGAGAGAGCTCAGCTCAGAGAGGCGCATGACAGATGGCGCA 4257
DB 5415 GTGTGGGATGTGGGGGCGAGAGAGCTCAGCTCAGAGAGGCGCATGACAGATGGCGCA 5474
QY 4258 TGGCAGATATCTTTCAGTGTGGCCAGTCCCAATGAAATCCAGTGGCCAGAGAGCCAG 4317
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DB 5655 GCTGCCAGGCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5714
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DB 5715 GAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5774
QY 4558 CGAGACAGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4617
DB 5775 CGAGACAGAGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5834
QY 4618 GCCAGAGAGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4677
DB 5835 GCCAGAGAGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5894
QY 4678 CAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4737
DB 5895 CAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5954
QY 4738 TGGGGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4797
DB 5955 TGGGGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6014
QY 4798 GGCCTCCCTGCTGCTGCTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4857
DB 6015 GGCCTC---CCTGCTCTCTCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6070
QY 4858 AGGAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4917
DB 6071 AGGAAAGCACA-CGATCACCTTCAAGTATTAATAAGTAATTTAGCTCTGAGAGCTTCAT 4917
QY 4918 TAGATTAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4957
DB 6130 TAGATTAGAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6129

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RESULT 5
ID AAA57484
AAA57484 standard; DNA; 5300 BP.

AC AAA57484;
XX
XX 20-OCT-2000 (first entry)
DT
XX
DE A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.
XX
XX TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;
KM

```

KM glaucoma; steroid sensitivity; progressive ocular hypertension;
KM vision loss; sr.
XX
OS Homo sapiens.
XX
FH Key
FH mutation
FT /tag= d
FT /note= "TIGRmt4 mutant"
FT /tag= a
FT /note= "TIGRmt1 mutant"
FT /note= "TIGRmt1 mutant"
FT /tag= b
FT /note= "TIGRmt2 mutant"
FT 4998
FT /tag= c
FT /note= "GTG added to produce TIGRmt3 mutant"
FT 5067.5073
FT CAAAT_signal
FT /tag= f
FT mutation
FT /tag= e
FT /note= "TIGRmt11 mutant"
FT 5230.5239
FT TATA_signal
FT /tag= g
PN MO200042220-A1.
PD 20-JUL-2000.
PD 20-JUL-2000.
PF 11-JAN-2000; 2000MO-US000559.
PF 11-JAN-1999; 99US-00227881.
PR 07-MAY-1999; 99US-00306828.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Nguyen TD, Polansky JR, Chen P, Chen H;
XX WPI; 2000-491060/43.
XX
XX Diagnosis, prognosis and treatment of glaucoma, based on detecting
XX specific polymorphisms in the promoter of the trabecular meshwork
XX inducible glucocorticoid receptor gene.
XX
XX Claim 34; Fig 1A-E; 122pp; English.
XX
XX The present sequence represents a TIGR (trabecular meshwork inducible
XX glucocorticoid receptor) promoter, isolated from an individual without
XX glaucoma. The specification describes a method for the diagnosis,
XX prognosis and treatment of glaucoma, based on detecting specific
XX polymorphisms in the promoter of the TIGR gene. The method is used for
XX diagnosis and prognosis of glaucoma (of all types), steroid sensitivity
XX and progressive ocular hypertension that leads to loss of vision.
XX Glaucoma can be treated by administering an agent that binds to cis-
XX acting elements within the TIGR promoter. The TIGR promoter (or other
XX regulatory regions) can be used to express homologous or heterologous
XX genes, particularly for tissue-specific expression of therapeutic
XX transgenes for treating glaucoma, also to generate transgenic animals and
XX in screening for compounds (specific modulators) with diagnostic or
XX therapeutic potential. Fragments of the TIGR sequence can be used as
XX amplification primers or probes, e.g. for isolating related sequences in
XX non-human animals
XX
SQ Sequence 5300 BP; 1482 A; 1152 C; 1235 G; 1431 T; 0 U; 0 Other;

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Query Match 67.8%; Score 4069.4; DB 3; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
QY 1 GCTCCACAGAGAGTCTCCCACTAGACTTTCATCAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 1216 GCTCCACAGAGAGTCTCCCACTAGACTTTCATCAGAGAGAGAGAGAGAGAGAGAGAG 1275

QY 61 CGTAGGGTGAAGGCTGTGTCTTACACCTAAGTATGCTTACACCTGAGCTCACTGC 120
 Db CGTAGGGTGAAGGCTGTGTCTTACACCTAAGTATGCTTACACCTGAGCTCACTGC 1335
 QY 121 AACCTGACCTCCGAGGTTCAAGCAATTCCTGTCTCAGGCTCCGCGAGTGGAGCT 180
 Db AACCTGACCTCCGAGGTTCAAGCAATTCCTGTCTCAGGCTCCGCGAGTGGAGCT 1395
 QY 181 ACAGCGCACGCGCCGCTAATTTTTGTATGTTAGTAGAGATGGGGTTTCAACATTTAG 240
 Db ACAGCGCACGCGCCGCTAATTTTTGTATGTTAGTAGAGATGGGGTTTCAACATTTAG 1455
 QY 1396 ACAGCGCACGCGCCGCTAATTTTTGTATGTTAGTAGAGATGGGGTTTCAACATTTAG 1455
 QY 241 CCGGCTGTGTCTTGAATCTCTGACCTCAGGTATCCACCCCACTCAGCTCTTAAAGTGC 300
 Db CCGGCTGTGTCTTGAATCTCTGACCTCAGGTATCCACCCCACTCAGCTCTTAAAGTGC 1515
 QY 301 TGGGATTTACAGGCAATGATGCAACGCGCCCGGCAAGGGTCAGTGTTTAAATGAAGATTAAC 360
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 QY 361 TTGAATGTTTACTAAACCAACAGGGAACAGACAAAAGCTGTGATTAATTTCAAGGATTC 420
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 Db TTGGATGGGAATGTGCCATGAGCTGCTGCTAGTCCAGACACTGTGCTCATCA 1636
 QY 481 CTTCCTTCCTCATCTCATTTTTCAGGCTAAGTTACATTTTATTCACCATGCTTTTGTG 540
 Db CTTCCTTCCTCATCTCATTTTTCAGGCTAAGTTACATTTTATTCACCATGCTTTTGTG 1696
 QY 541 GTAAGCTTCAATCTGTACTGAATAAAGATATACATTAACCTAGTTCAATTTGGAGCCA 600
 Db GTAAGCTTCAATCTGTACTGAATAAAGATATACATTAACCTAGTTCAATTTGGAGCCA 1756
 QY 601 TCTGTGTGTGTATTAAGGGAGAGAGGCAATCCCAAGACCTCTTGAAGCCCGCGGAG 660
 Db TCTGTGTGTGTATTAAGGGAGAGAGGCAATCCCAAGACCTCTTGAAGCCCGCGGAG 1816
 QY 661 AGGTTTCCTCTCAGCTGGGGAGCCCTGCAAGACCCGCGGTCTGTGGTGTCTGAACA 720
 Db AGGTTTCCTCTCAGCTGGGGAGCCCTGCAAGACCCGCGGTCTGTGGTGTCTGAACA 1876
 QY 721 ACCTCCAGCCCGTGCACATGCTGTGTGTATCACTCTTGAAGGACCTGTGCTTTCT 780
 Db ACCTCCAGCCCGTGCACATGCTGTGTGTATCACTCTTGAAGGACCTGTGCTTTCT 1936
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 Db ATTTCTGTGTACTGTTTATTCATTCAGGCAATTCATTTGAACAATTTATTTGATTAATA 1996
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 Db TCTGCAGACACAGAGCAAAATGGTGAAGCAAGGACCTGACCTTCTGTGAG 2056
 QY 901 GTGAACGTTTCTCATGAAGAAGTGCAGAAATTAATTAAGCCAGCCAACTTAAACCA 960
 Db GTGAACGTTTCTCATGAAGAAGTGCAGAAATTAATTAAGCCAGCCAACTTAAACCA 2116
 QY 961 GTGTGAAGAAAGAAATTAACACATCTTTGAAGATTTGTGGCGACATCCCTTAAACA 1020
 Db GTGTGAAGAAAGAAATTAACACATCTTTGAAGATTTGTGGCGACATCCCTTAAACA 2176
 QY 1021 GGGCACTCTCCTAGGGCCCGCTGTGCATCCATGTCGCGGAGGCCCAAGCCCGAGT 1080
 Db GGGCACTCTCCTAGGGCCCGCTGTGCATCCATGTCGCGGAGGCCCAAGCCCGAGT 2236
 QY 1081 CTTCGAAGCTCTCTCTCATCATGATCAAGCGCTGAGCTGGCTGTGCTTCCGCTG 1140
 Db CTTCGAAGCTCTCTCTCATCATGATCAAGCGCTGAGCTGGCTGTGCTTCCGCTG 2296

QY 1141 AATGCTCTGTGTCATCTGAGCTGAGACTCTTTGCTCCAGGCTCCAGAAAGAAATGG 1200
 Db AATGCTCTGTGTCATCTGAGCTGAGACTCTTTGCTCCAGGCTCCAGAAAGAAATGG 2356
 QY 1201 AGAGGAAACTTACTTCAACGAGAAATCTGAGGGGACAGTGTCTTCTCAGAGGGAAGGG 1260
 Db AGAGGAAACTTACTTCAACGAGAAATCTGAGGGGACAGTGTCTTCTCAGAGGGAAGGG 2416
 QY 1261 GCGTCCACGTCAGAGAAATTTCCAGAGGTGGGACCTGACAGGAGTGGGACGCTGGGC 1320
 Db GCGTCCACGTCAGAGAAATTTCCAGAGGTGGGACCTGACAGGAGTGGGACGCTGGGC 2476
 QY 1321 TGAACGGGTCTGAAAGCAGAAAGTGAAGAGGCAAGCTGAAGTCCACAGATGTTTC 1380
 Db TGAACGGGTCTGAAAGCAGAAAGTGAAGAGGCAAGCTGAAGTCCACAGATGTTTC 2536
 QY 1381 AGTGTGTTCACGGGCTGGGAATTTTCCGTGCTTCCGTGAGCCCTTTATCTTTCT 1440
 Db AGTGTGTTCACGGGCTGGGAATTTTCCGTGCTTCCGTGAGCCCTTTATCTTTCT 2596
 QY 1441 CTGCTTGAAGAGAAAGATCTATTTGATGAAGGATGACATTAAGTCAAGCTGTT 1500
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 QY 1501 AAAATTCAGGAGTGTGATGAGTTTCTTCAAGAGCCCTTTATTTAATGGAAATATAG 1560
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 QY 1561 GAAGCGAGCTCATTTCTAGGCGCTTAATTCACGGAAGAGTGACTGGAAGCTTTCTTT 1620
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 QY 1621 CATGCTTTGGGGAACATCACTCAGCCGCTGTGGAATTTGGCTATGCAAGACGTCGAA 1680
 Db CATGCTTTGGGGAACATCACTCAGCCGCTGTGGAATTTGGCTATGCAAGACGTCGAA 2836
 QY 1681 AACCTTGAATCAGAGACCTGAGTTTCTTCTGTGCTTCAGATTTGTTGGCTGTGAC 1740
 Db AACCTTGAATCAGAGACCTGAGTTTCTTCTGTGCTTCAGATTTGTTGGCTGTGAC 2896
 QY 1741 CGTGGCAAGTGTCTCTCTTCCCTGGGCCATATCTTTCTTGCTATTAACCTTGCA 1800
 Db CGTGGCAAGTGTCTCTCTTCCCTGGGCCATATCTTTCTTGCTATTAACCTTGCA 2956
 QY 1801 GCTCTCGTGTCTGTGAACATTCCTCGTGTATCTCTGTGAGGGGAGTGTGAAGGGG 1860
 Db GCTCTCGTGTCTGTGAACATTCCTCGTGTATCTCTGTGAGGGGAGTGTGAAGGGG 3016
 QY 1861 AAGAGCAGAGCTGAGCACTGAGCCACAGGGAGGTGAGGGGACAGAAAGGCAAG 1920
 Db AAGAGCAGAGCTGAGCACTGAGCCACAGGGAGGTGAGGGGACAGAAAGGCAAG 3076
 QY 1921 CAGAACTGGGTGCTCATCAGTCTCTCATGTATCACGTCAACATCTCCAGAACCGAGGCA 1980
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 QY 2161 TGAACGACACCCCAAGCGCTGACAGTGAAGTGTGACAGCAGGAGTGAACCTGACGCG 2220
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 QY 2521 AGGCAATCCCGTTCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
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 Db 3796 TCAAGCTTACGTTCTGCTGATATATGATGTTGTTTTGAGAGAGAGAGAGAG 3855
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 Db 3856 TACTATCTGATTCAG 3915
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 QY 2761 AGAGCAATCTGTTCTTCACCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
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 QY 2821 ACTTCAGAGATTCAGCTGTTGTTGTTATTAACAACATTAAGTTCCTCAAGGCAATC 2880
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 Db 4396 GTTGTGAGATACGTTGTTAAGTAAATTTATGCTCAAACTCTTGAATTAAGAGAG 4455
 QY 3241 TCTGCTGAGATCTGTTTAACTATTAATTAATTAATTAATTAATTAATTAATTA 3300
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 Db 4576 TCTTTCTGAGAGAGAGTTCCCAAGTTTCAACCAATGAGGTTCTTGGCATGACACAG 4635
 QY 3421 AGTAAAGATCTGATTTAGAGGCTTAACATGACATTTGGGCTGAGAGAGAGAGAG 3480
 Db 4636 AGTAAAGATCTGATTTAGAGGCTTAACATGACATTTGGGCTGAGAGAGAGAGAG 4695
 QY 3481 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGAGAGAGAGAGAGAGAG 3540
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 Db 4936 ACTAAGATATATCTCTGTTGAATACAGACACAGTACCTCTGTTAAGTGTGTAC 4995
 QY 3781 --GT 3838
 Db 4996 GT 5055
 QY 3839 GGTATGAGTGCATTAATTTGGATGTTCTTTTAAAGAGAGAGAGAGAGAGAGAGAG 3898
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 QY 3899 AAGTTATTTTCTAAGATCTTGTGAGAGGTTGAAGGACCCCTGTGTGACAGAGCC 3958
 Db 5116 AAGTTATTTTCTAAGATCTTGTGAGAGGTTGAAGGACCCCTGTGTGACAGAGCC 5175
 QY 3959 ACCGAGCTCAGAGGAG 4018
 Db 5176 ACCGAGCTCAGAGGAG 5235
 QY 4019 TAACTCTCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4078
 Db 5236 TAACTCTCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5295
 QY 4079 ACAGC 4083
 Db 5296 ACAGC 5300
 RESULT 6
 ADF13152 standard; DNA; 5300 BP.
 ID ADF13152 standard; DNA; 5300 BP.
 XX ADF13152;
 AC 12-PEB-2004 (first entry)
 XX 12-PEB-2004 (first entry)
 DT Human TIGR promoter DNA.
 XX Human TIGR promoter DNA.
 DE ds; human; glaucoma; TIGR; promoter; inherited glaucoma;
 KW primary open angle glaucoma; intraocular pressure;
 KW visual field loss risk increase.
 OS Homo sapiens.
 XX Homo sapiens.
 XX US2003119000-A1.
 XX

PD 26-JUN-2003.
 XX 05-NOV-2001; 2001US-00985637.
 XX 05-NOV-2001; 2001US-00985637.
 PR (POLA/) POLANSKY J.
 XX Polansky J;
 PI WPI; 2004-031252/03.
 PT Treatment of glaucomatous patient comprises administering non-steroidal
 XX anti-inflammatory drug to patient.
 PS Disclosure; SEQ ID NO 1; 32pp; English.
 CC The invention relates to a method of treating glaucomatous patient
 CC comprising determining whether the patient has a mutation in the TIGR
 CC promoter consisting of TIGRm1 and/or TIGRm11 and administering a non-
 CC steroidal anti-inflammatory drug to the patient. The method is useful for
 CC the treatment of a glaucomatous patient, i.e. patient having glaucoma,
 CC e.g. inherited glaucoma, or primary open angle glaucoma. The method
 CC allows the identification of individuals at risk for progressive
 CC increases in intraocular pressure, which is a risk factor for glaucoma.
 CC It also allows the identification of individuals among ocular
 CC hypertensive/glaucoma suspect groups at increased risk of visual field
 CC loss. The present sequence represents the human TIGR promoter DNA.
 SQ Sequence 5300 BP; 1482 A; 1152 C; 1235 G; 1431 T; 0 U; 0 Other;
 Query Match 67.8%; Score 4069.4; DB 12; Length 5300;
 Best local similarity 99.9%; Pred. No. 0;
 Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
 QY 1 GCTCCACAGGAAGTCTCCCACTTAGAATTCTGATCAAGATGTTACAGCCAGAACTC 60
 DB 1216 GCTCCACAGGAAGTCTCCCACTTAGAATTCTGATCAAGATGTTACAGCCAGAACTC 1275
 QY 61 CGTAGGGGTGAGGGTCTGTGTCTTACACCTACCTTAAGTCTTAACCTGAGCTCACTGC 120
 DB 1276 CGTAGGGGTGAGGGTCTGTGTCTTACACCTACCTTAAGTCTTACACCTGAGCTCACTGC 1335
 QY 121 AACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTAGCTCCCGAGTGGAGT 180
 DB 1336 AACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTAGCTCCCGAGTGGAGT 1395
 QY 181 ACAGGCGCACGCGCCGAGCTAATTTTGTATTTAGTAGAGATGGGGTTTCAACATATTAG 240
 DB 1396 ACAGGCGCACGCGCCGAGCTAATTTTGTATTTAGTAGAGATGGGGTTTCAACATATTAG 1455
 QY 241 CCGGCTGTCTTGAATCTCCGACCTCAAGTATCAACCACTCAAGCTCTTAAGTGC 300
 DB 1456 CCGGCTGTCTTGAATCTCCGACCTCAAGTATCAACCACTCAAGCTCTTAAGTGC 1515
 QY 301 TGGGATTACAGGATAGTCAACGCGCCCGGCAAGGTCAGTGTATTATAAGATAAC 360
 DB 1516 TGGGATTACAGGATAGTCAACGCGCCCGGCAAGGTCAGTGTATTATAAGATAAC 1575
 QY 361 TTGAATGTTTAACTAAACCAAGGAAACAGACAAAGCTGTATTAATTTCAAGGATTC 420
 DB 1576 TTGAATGTTTAACTAAACCAAGGAAACAGACAAAGCTGTATTAATTTCAAGGATTC 1635
 QY 421 TTGGGATGGGGAATGGTGCATAGAGTGTGCTGCTAGTCCAGACACATGCTTCATCA 480
 DB 1636 TTGGGATGGGGAATGGTGCATAGAGTGTGCTGCTAGTCCAGACACATGCTTCATCA 1695
 QY 481 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTAACTATTATTCACATGCTTTTGG 540
 DB 1696 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTAACTATTATTCACATGCTTTTGG 1755
 QY 541 GTAAGCTTCACATCTTAACTGAATTAAGATTAATTAATTAATTTCAATTTGGGGCA 600
 DB |||||

DB 1756 GTAAGCTTCACATCTTAACTGAATTAAGATTAATTAATTAATTTCAATTTGGGGCA 1815
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 DB 1816 TCTGTGTGTGTATATAGGAGAGGAGCATATCCAGAGACTCTTTGAAGCCCGGAG 1875
 QY 661 AGGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTCTTGAGCA 720
 DB 1876 AGGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTCTTGAGCA 1935
 QY 721 ACCTGCAGCCCGTGCACATGTTTGTATATCACTCTAGAGGACCTGTGCTTCT 780
 DB 1936 ACCTGCAGCCCGTGCACATGTTTGTATATCACTCTAGAGGACCTGTGCTTCT 1995
 QY 781 ATTTCTGTGTGATCTGTTCAATTCACAGGACATTCATGACAAATTTATAGTACTATA 840
 DB 1996 ATTTCTGTGTGATCTGTTCAATTCACAGGACATTCATGACAAATTTATAGTACTATA 2055
 QY 841 TCTGCAGACACACAGACAAATATGTAGCAAAAGCATGCTGCTTACCTTCTGAG 900
 DB 2056 TCTGCAGACACACAGACAAATATGTAGCAAAAGCATGCTGCTTACCTTCTGAG 2115
 QY 901 GTGACATTTCTCATGGAAGACGTGCAGAAAGAAATTAATAGCCAGCACTTAAACCA 960
 DB 2116 GTGACATTTCTCATGGAAGACGTGCAGAAAGAAATTAATAGCCAGCACTTAAACCA 2175
 QY 961 GTGCTGAAGAAAGAAATTAACACATCTTGAAGAAATTTGTCAGACATCTTAACAA 1020
 DB 2176 GTGCTGAAGAAAGAAATTAACACATCTTGAAGAAATTTGTCAGACATCTTAACAA 2235
 QY 1021 GGGCACTCCCTAGCGCCCTGCTGCTCATGTGTCGGAGAGCCCGCAAGCCGAGT 1080
 DB 2236 GGGCACTCCCTAGCGCCCTGCTGCTCATGTGTCGGAGAGCCCGCAAGCCGAGT 2295
 QY 1081 CTTTCAAGCTCCCTCCCTCAATCAAGTCAAGGCTGCACTGGCTGCTGCTTCCGGT 1140
 DB 2296 CTTTCAAGCTCCCTCCCTCAATCAAGTCAAGGCTGCACTGGCTGCTGCTTCCGGT 2355
 QY 1141 AATGCTCTGGTGCATGAGCTGAGACTGCTTGTGCTTCCAGGCTCCAGAAAGAAATGG 1200
 DB 2356 AATGCTCTGGTGCATGAGCTGAGACTGCTTGTGCTTCCAGGCTCCAGAAAGAAATGG 2415
 QY 1201 AGAGGAAACTAGTCTTAACGAGAAATCTGAGGGGACAGTGTCTTCAAGGAAAGGG 1260
 DB 2416 AGAGGAAACTAGTCTTAACGAGAAATCTGAGGGGACAGTGTCTTCAAGGAAAGGG 2475
 QY 1261 GCTTCCAGTCCAGAGAAATTCAGAGGTGGGACCTGCAGAGGAGTGGGAGCGCTGGGGC 1320
 DB 2476 GCTTCCAGTCCAGAGAAATTCAGAGGTGGGACCTGCAGAGGAGTGGGAGCGCTGGGGC 2535
 QY 1321 TGAAGGGGTGCTGAAGGCAAGGATGAAGGAGGCAAGGCTGAAGGCTGCCAGATGTT 1380
 DB 2536 TGAAGGGGTGCTGAAGGCAAGGATGAAGGAGGCAAGGCTGAAGGCTGCCAGATGTT 2595
 QY 1381 AGTGTGTTTCAAGGGGCTGGAGATTTTCCGTGCTTCTGTGAGCTTTTATCTTTTCT 1440
 DB 2596 AGTGTGTTTCAAGGGGCTGGAGATTTTCCGTGCTTCTGTGAGCTTTTATCTTTTCT 2655
 QY 1441 CTGCTTGAAGAGAAAGATCTAATTTCAAGAGGATGCAATTTCAATAAGTCACTGT 1500
 DB 2656 CTGCTTGAAGAGAAAGATCTAATTTCAAGAGGATGCAATTTCAATAAGTCACTGT 2715
 QY 1501 AAAATTTCAAGGATGTCATGGGATTTTCTTCAAGAGGCTTTTATATGGGATATAG 1560
 DB 2716 AAAATTTCAAGGATGTCATGGGATTTTCTTCAAGAGGCTTTTATATGGGATATAG 2775
 QY 1561 GAAGGAGCTCATTTCTAGGCGCTTAATTTCAAGAGAGTGACTGAGTCTTTTCTTT 1620
 DB 2776 GAAGGAGCTCATTTCTAGGCGCTTAATTTCAAGAGAGTGACTGAGTCTTTTCTTT 2835
 QY 1621 CATGCTTCTGAGCAACTCAAGCCCTGTGTGTGAATTGGCTTAATGCAAGCGTGGAA 1680
 DB 2836 CATGCTTCTGAGCAACTCAAGCCCTGTGTGTGAATTGGCTTAATGCAAGCGTGGAA 2895


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Db 5056 GCGTATGGCTCAATAATGGAGATCTTTTAAAAAGAACTCAAGACGCTTCGG 5115
Qy 3889 AAGTTATTTTCTAAGATCTTCTGCGACGCTGAAGCAACCCCTGTGCACAGCCCC 3958
Db 5116 AAGTTATTTTCTAAGATCTTCTGCGACGCTGAAGCAACCCCTGTGCACAGCCCC 5175
Qy 3959 ACCGAGCTCAAGTGGGCACTCTGTCTTCCCAATGAAGGGCTGCTCCCACTATATA 4018
Db 5176 ACCGAGCTCAAGTGGGCACTCTGTCTTCCCAATGAAGGGCTGCTCCCACTATATA 5235
Qy 4019 TAAACCTCTGAGCTGAGCGATGAGCCAGCAAGGCCCATCTCAGGCACTCTCAGC 4078
Db 5236 TAAACCTCTGAGCTGAGCGATGAGCCAGCAAGGCCCATCTCAGGCACTCTCAGC 5295
Qy 4079 ACAGC 4083
Db 5296 ACAGC 5300

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RESULT 7
ADQ15241
ID ADQ15241 standard; DNA; 5300 BP.
AC ADQ15241;
DT 23-SEP-2004 (first entry)
DE Human trabecular meshwork glucocorticoid response, TIGR, 5' region.
XX Human; de; trabecular meshwork glucocorticoid response; TIGR, 5' region;
XX glaucoma; SNP; single nucleotide polymorphism;
XX non-steroidal anti-inflammatory drug; NSAID; intraocular pressure;
XX inherited glaucoma; open angle glaucoma; primary open angle glaucoma;
XX ocular inflammation.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT replacement(4337,G)
XX FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
FT variation replacement(5113,C)
FT /*tag= b
FT /standard_name= "single nucleotide polymorphism"
XX US2004132795-A1.
XX 08-JUL-2004.
XX 22-DEC-2003; 2003US-00741339.
XX 05-NOV-2001; 2001US-00985637.
XX (POLA/) POLANSKY J.
XX PA
XX PI Polansky J;
XX WPI; 2004-542638/52.
XX
XX Treatment of glaucomatous patient involves determining whether patient
XX has a mutation in trabecular meshwork glucocorticoid response promoter,
XX followed by administration of non-steroidal anti-inflammatory drug.
XX
XX Disclosure; SEQ ID NO 1; 31pp; English.
XX
XX The invention relates to a method of providing treatment to a
XX glaucomatous patient involves (a) determining whether the patient has a
XX mutation in the trabecular meshwork glucocorticoid response (TIGR)
XX promoter selected from TIGRm1, TIGRm11, or both TIGRm1 and TIGRm11
XX and (b) administering a non-steroidal anti-inflammatory drug (NSAID) to
XX the patient. Also included are a method of preventing increases in
XX intraocular pressure in a patient predisposed to developing glaucoma, a

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CC method for decreasing the mean diurnal intra-ocular pressure in a
CC patient, a method of providing treatment to a patient known to possess at
CC least one mutation in the TIGR gene selected from TIGRm1 and TIGRm11,
CC a method of selecting a patient for a clinical trial, a method of
CC improving the results of a drug study involving a treatment for elevated
CC intraocular pressure, a method of determining whether a patient is at
CC risk for developing elevated intraocular pressure, and a method of
CC testing the efficacy of a therapeutic agent at counteracting glaucoma
CC pathogenic mechanisms. The methods are used for preventing increases in
CC intraocular pressure in a patient (i.e. a patient having asymptomatic
CC glaucoma) predisposed to developing glaucoma (such as an inherited
CC glaucoma, an open angle glaucoma (e.g. primary open angle glaucoma), for
CC decreasing the mean diurnal intra-ocular pressure in a patient and the
CC treatment of ocular inflammation. The method allows the identification of
CC individuals at risk for progressive increase in intraocular pressure and
CC thus allows the identification of individuals among ocular
CC hypertensive/glaucoma suspect groups at increased risk of visual field
CC loss. The present sequence is the 5' region of the human TIGR gene.
XX
XX
SQ Sequence 5300 BP; 1482 A; 1152 C; 1235 G; 1431 T; 0 U; 0 Other;

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Query Match 67.8%; Score 4069.4; DB 12; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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Qy 1 GCTCCAGAGAAAGTCTCCCACTAGACTTTCGATCAGCATGTATCAAGCCAGAAAGCTC 60
Db 1216 GCTCCAGAGAAAGTCTCCCACTAGACTTTCGATCAGCATGTATCAAGCCAGAAAGCTC 1275
Qy 61 CGTAGAGGTAGAGGTCTGTGTCTTACACTTACTGATGCTTACACCTGAGCTCACTGC 120
Db 1276 CGTAGAGGTAGAGGTCTGTGTCTTACACTTACTGATGCTTACACCTGAGCTCACTGC 1335
Qy 121 AACCTGCTCCCAAGGTTCAGCAATTCCTGCTCAGCTCCCGGTAGCTGGAGCT 180
Db 1336 AACCTGCTCCCAAGGTTCAGCAATTCCTGCTCAGCTCCCGGTAGCTGGAGCT 1395
Qy 181 ACAGGCGCAGCCCGGCTAATTTTGTATTGTATTAGATAGGAGTTTACCATATTAG 240
Db 1396 ACAGGCGCAGCCCGGCTAATTTTGTATTGTATTAGATAGGAGTTTACCATATTAG 1455
Qy 241 CCCGAGTGTCTTGAACCTCTGACCTGAGTATCCACCCACTGACGCTCTTAAAGTGC 300
Db 1456 CCCGAGTGTCTTGAACCTCTGACCTGAGTATCCACCCACTGACGCTCTTAAAGTGC 1515
Qy 301 TGGGATTCAGGCAATGATGCCCGGCCGCAAGGGTCAAGTTTATTAAGGAATAC 360
Db 1516 TGGGATTCAGGCAATGATGCCCGGCCGCAAGGGTCAAGTTTATTAAGGAATAC 1575
Qy 361 TTGAATGTTTACTTAAACCAACAGGAAACAGACAAAAGCTGTATTAATTCAGGAAATTC 420
Db 1576 TTGAATGTTTACTTAAACCAACAGGAAACAGACAAAAGCTGTATTAATTCAGGAAATTC 1635
Qy 421 TTGGATGGGGAATGATGATGAGCTGCTGCTAGTCCCAAGCACTGCTCTATCA 480
Db 1636 TTGGATGGGGAATGATGATGAGCTGCTGCTAGTCCCAAGCACTGCTCTATCA 1695
Qy 481 CTTTCTTCCCTCATTCCTATTTTCAAGGTAGTTACATTTTATTCACCAAGCTTTTGTG 540
Db 1696 CTTTCTTCCCTCATTCCTATTTTCAAGGTAGTTACATTTTATTCACCAAGCTTTTGTG 1755
Qy 541 GTAAGCCTGCACATGTTACTGAATAATAGATATACATTAATGTTTCTTGGAGCA 600
Db 1756 GTAAGCCTGCACATGTTACTGAATAATAGATATACATTAATGTTTCTTGGAGCA 1815
Qy 601 TCTGTGTGTGTATAGAGGAGAGAGGAGATACCCCAAGACTCTTGAAGCCCCCGAG 660
Db 1816 TCTGTGTGTGTATAGAGGAGAGAGGAGATACCCCAAGACTCTTGAAGCCCCCGAG 1875
Qy 661 AGGTTTCTCTTCAGCTGGGGAGAGCCCTGCAAGCAACCCGGGGTCTGGGGTCTCCGAGCA 720
Db 1876 AGGTTTCTCTTCAGCTGGGGAGAGCCCTGCAAGCAACCCGGGGTCTGGGGTCTCCGAGCA 1935

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QY	721	ACCTGCACGCCGCTGCACCTGGTGTGTTTGTATATCACTCTCAGAGGACCTGTGTTCT	780
Db	1936	ACCTGCACGCCGCTGCACCTGGTGTGTTTGTATATCACTCTCAGAGGACCTGTGTTCT	1995
QY	781	ATTTCGTGTGACTGTTCATTCTATCCAGGCAATTCATTGACCAATTTATAGTACTTTATA	840
Db	1996	ATTTCGTGTGACTGTTCATTCTATCCAGGCAATTCATTGACCAATTTATAGTACTTTATA	2055
QY	841	TCTGCCAGACACACAGAGCAAAATGTGTAGCAAAAGCACTGTGCTTACCTTCGTGAG	900
Db	2056	TCTGCCAGACACACAGAGCAAAATGTGTAGCAAAAGCACTGTGCTTACCTTCGTGAG	2115
QY	901	GTGACAGTTTCTCATGGAAGAGTGTACAGAAATAATATAGCCGCACTTTAAACCA	960
Db	2116	GTGACAGTTTCTCATGGAAGAGTGTACAGAAATAATATAGCCGCACTTTAAACCA	2175
QY	961	GTGCTGAAAGAAAGAAATTAACACATCTTGAAATAATGTGCGAGCATCCCTTAACA	1020
Db	2176	GTGCTGAAAGAAAGAAATTAACACATCTTGAAATAATGTGCGAGCATCCCTTAACA	2235
QY	1021	GGCCACCTCCCTTAGGCCCCCTGTCTGCTCCATCTGTGCCGAGGCCCCCAAGCCGAGT	1080
Db	2236	GGCCACCTCCCTTAGGCCCCCTGTCTGCTCCATCTGTGCCGAGGCCCCCAAGCCGAGT	2295
QY	1081	CTTCCAAAGCCTCTCTCTCCATCATGTCACAGGCTGCACTGGCTGCTCGTTCCTG	1140
Db	2296	CTTCCAAAGCCTCTCTCTCCATCATGTCACAGGCTGCACTGGCTGCTCGTTCCTG	2355
QY	1141	AATGCTCTGTGAGCATCTGAGCTGTGAGACTCCTTGGCTTCAGAGCTCCAGAAAGAAATG	1200
Db	2356	AATGCTCTGTGAGCATCTGAGCTGTGAGACTCCTTGGCTTCAGAGCTCCAGAAAGAAATG	2415
QY	1201	AGAGGAAACTAGTCTTAACGAGAAATCTGAGAGGGGACAGTGTTCCTCAGAGGGAAAGG	1260
Db	2416	AGAGGAAACTAGTCTTAACGAGAAATCTGAGAGGGGACAGTGTTCCTCAGAGGGAAAGG	2475
QY	1261	GCTTCACAGTCCAGGAAATTCAGGAGGTGGGACATCCAGAGAGTGGGGACGTGGGGC	1320
Db	2476	GCTTCACAGTCCAGGAAATTCAGGAGGTGGGACATCCAGAGAGTGGGGACGTGGGGC	2535
QY	1321	TGAGCGGGTGTGCTGAAGGCGAGGAAGGTGAAAGGGCAGGCTGAAGCTGCCAGATGTT	1380
Db	2536	TGAGCGGGTGTGCTGAAGGCGAGGAAGGTGAAAGGGCAGGCTGAAGCTGCCAGATGTT	2595
QY	1381	AGTGTGTTCAAGGGGCTGGGAGTATTCGATGCTCTCTGAGGCTTTTATCTTTCT	1440
Db	2596	AGTGTGTTCAAGGGGCTGGGAGTATTCGATGCTCTCTGAGGCTTTTATCTTTCT	2655
QY	1441	CTGCTTGAGAGAGAAAGTCTATTTCTATTCAGAGGAGATGCACTTTCATTAAGTCACTGT	1500
Db	2656	CTGCTTGAGAGAGAAAGTCTATTTCTATTCAGAGGAGATGCACTTTCATTAAGTCACTGT	2715
QY	1501	AAAATTCAGAGGTGTGCATGGGTTTTCTTCAACGAGGCTTTATTTATATGGAAATATAG	1560
Db	2716	AAAATTCAGAGGTGTGCATGGGTTTTCTTCAACGAGGCTTTATTTATATGGAAATATAG	2775
QY	1561	GAAGCGAGCTCATTTTCCTAGGCGGTTAATTCAGCGAAGAAATGACGTGAGCTTTCTT	1620
Db	2776	GAAGCGAGCTCATTTTCCTAGGCGGTTAATTCAGCGAAGAAATGACGTGAGCTTTCTT	2835
QY	1621	CATGTCTTCTGGGCAACTACTCAGCCCTGTGTGGAATTTGACTTATGCAAGCGTGCAA	1680
Db	2836	CATGTCTTCTGGGCAACTACTCAGCCCTGTGTGGAATTTGACTTATGCAAGCGTGCAA	2895
QY	1681	AACCTTGAAATCAGAGAACTCGGTTTTCTTCTGTGTTCTGCAATTTGGTGTGTGAGC	1740
Db	2896	AACCTTGAAATCAGAGAACTCGGTTTTCTTCTGTGTTCTGCAATTTGGTGTGTGAGC	2955
QY	1741	CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGTGCTATTTAAACCCCTTGA	1800
Db	2956	CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGTGCTATTTAAACCCCTTGA	3015
QY	1801	GCTCTCGTGTCTGTAAACCTTCCCTGTGTATCTCTGTGAGGGGGAGTTGTAGAGGGG	1860

Db	3016	GCTCTCGTGTCTGTGAACTCTCCCTGTGATTTCTCTGTGAGGGGGGATGTTTGAGAGGGG	3075
OY	1861	AAGGAGGCAAGCTGAGACACTGACCAAGGAGGAGGTGAGGGGGGACAGAAAGGCAGG	1922
Db	3076	AAAGAGGCAAGAGCTGTGAGACACTGAGCCAGGAGGAGGTGAGGGGGACAGAAAGGCAGG	3135
OY	1921	CAGAAAGCTGGGTGCTCCATCAAGTCCCTCACTGATCAAGCTTCAGAGCTCCAGAGCCAGCA	1980
Db	3136	CAGAAAGCTGGGTGCTCCATCAAGTCCCTCACTGATCAAGCTTCAGAGCTCCAGAGCCAGCA	3199
OY	1991	CAATGCTTCAGAGAAAGCTCAATGAAACCCAAAGCCACATTTTCTTCCCTTAAGCAATGAC	2040
Db	3196	CAATGCTTCAGAGAAAGCTCAATGAAACCCAAAGCCACATTTTCTTCCCTTAAGCAATGAC	3255
OY	2041	AATGGCAATTTGSCAAATAACCAAAAAAGATGACAGAGCAATACGAGTGGTAGTCTTTTGCCGT	2100
Db	3256	AATGGCAATTTGSCAAATAACCAAAAAAGATGACAGAGCAATACGAGTGGTAGTCTTTTGCCGT	3315
OY	2101	GCATTTCAAAAACTGGGCGACAGCAAGTGGAAAAATGCGAGATGTTTAACTTTTCAACC	2166
Db	3316	GCATTTCAAAAACTGGGCGACAGCAAGTGGAAAAATGCGAGATGTTTAACTTTTCAACC	3375
OY	2161	TGACCAAGACCCCAACGAGCTCAGCAGTGACTGCTGACAGCAGAGTGAACCTGCAAGGC	2220
Db	3376	TGACCAAGACCCCAACGAGCTCAGCAGTGACTGCTGACAGCAGAGTGAACCTGCAAGGC	3435
OY	2221	AGGGAGGAGAGAAAAAGAGAGGAGTAAGTATAGACCAAGAAAGACAGATTCAATTCAG	2280
Db	3436	AGGGAGGAGAGAAAAAGAGAGGAGTAAGTATAGACCAAGAAAGACAGATTCAATTCAG	3499
OY	2281	GGCAGTGGGAATTTGACCAACGAGGATTTATAGTCCAGTGAATCTGGGTTCTTAGAGGCAAG	2340
Db	3496	GGCAGTGGGAATTTGACCAACGAGGATTTATAGTCCAGTGAATCTGGGTTCTTAGAGGCAAG	3555
OY	2341	GCTATATTGTGGGGGGAAAAAATCAGTTCAAGGAGTCGGAGACCTGATTTCTAATAC	2400
Db	3556	GCTATATTGTGGGGGGAAAAAATCAGTTCAAGGAGTAACGGGAGACCTGATTTCTAATAC	3615
OY	2401	TATATTTTTCCTTTTACAAGCTGAGTATTTCTGAGCAAGTCAACAGATAGTATCTGAGGCT	2460
Db	3616	TATATTTTTCCTTTTACAAGCTGAGTATTTCTGAGCAAGTCAACAGATAGTATCTGAGGCT	3675
OY	2461	GTAAGATTACTAGTATCTCTCTTATTTAGAACTGTTTTCTCTGTGAGTTAGCAGACA	2520
Db	3676	GTAAGATTACTAGTATCTCTCTTATTTAGAACTGTTTTCTCTGTGAGTTAGCAGACA	3735
OY	2521	AGGGCAATCCCGTTCTTTTAAACAGAAAGAAACATTCCTAAGATAAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCCGTTCTTTTAAACAGAAAGAAACATTCCTAAGATAAAGCCAAACAGAT	3795
OY	2581	TCAAGCTAGTCTTCTGCTGACTATATGATTTGTTTTTGAAAAATCAATTCAGCGATGT	2640
Db	3796	TCAAGCTAGTCTTCTGCTGACTATATGATTTGTTTTTGAAAAATCAATTCAGCGATGT	3855
OY	2641	TACTATCTGATTCAGAAATAGAGACTAGTAAACCTTTGGTGCAGCTGTAAACAAACCCAT	2700
Db	3856	TACTATCTGATTCAGAAATAGAGACTAGTAAACCTTTGGTGCAGCTGTAAACAAACCCAT	3915
OY	2701	TTGTAAATGTCTCAAGTTCAAGGCTTAACTGCAGAACCAATCAATAATAGATAGATCTTT	2760
Db	3916	TTGTAAATGTCTCAAGTTCAAGGCTTAACTGCAGAACCAATCAATAATAGATAGATCTTT	3975
OY	2761	AGAGCAAACTGTGTTTTTCTCACTCTGTGAGGTGAGTCTGCAAGGCAAGTTGGAAATATTT	2820
Db	3976	AGAGCAAACTGTGTTTTTCTCACTCTGTGAGGTGAGTCTGCAAGGCAAGTTGGAAATATTT	4035
OY	2821	ACTTCAACAAGTATTTGACACTGTGTTGGTATTTAACAACAATAAAGTTGCTCAAAAGGCATC	2880
Db	4036	ACTTCAACAAGTATTTGACACTGTGTTGGTATTTAACAACAATAAAGTTGCTCAAAAGGCATC	4095
OY	2881	ATTATTTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATATTTATTTGGCTATTTGCC	2940

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Db      4096 ATTATTCAGAGTGGCTTAAAGTTACTTCGACAGTTTTGTATATTATGGCTATAGCC 4155
Qy      2941 ATTTGCTTTTGGTTTCTCTTGGGTTTATTAATGAAAGAGGATTTAACTTAC 3000
Db      4156 ATTTGCTTTTGGTTTCTCTTGGGTTTATTAATGAAAGAGGATTTAACTTAC 4215
Qy      3001 AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTACATTTTGTTTTACACCTT 3060
Db      4216 AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTACATTTTGTTTTACACCTT 4275
Qy      3061 CTAACTAAATTTTAACTTTTATTCATTCGCAATAGACCATAAATCTAAAGTGTATTA 3120
Db      4276 CTAACTAAATTTTAACTTTTATTCATTCGCAATAGACCATAAATCTAAAGTGTATTA 4335
Qy      3121 ACAGTACCTGTGATTTGTCAATTACCAATAGAAATCAGACATTTTATGATATTTACA 3180
Db      4336 ACAGTACCTGTGATTTGTCAATTACCAATAGAAATCAGACATTTTATGATATTTACA 4395
Qy      3181 GTTGTGACAGATACCTGTGAAGTGAATTTATTAAGTAACTTCTTGAATTTAGACC 3240
Db      4396 GTTGTGACAGATACCTGTGAAGTGAATTTATTAAGTAACTTCTTGAATTTAGACC 4455
Qy      3241 TCTCTGTGATCTGTTTAACTATTAATTAATTAATTAATTAATTTGATATTTTGA 3300
Db      4456 TCTCTGTGATCTGTTTAACTATTAATTAATTAATTAATTAATTTGATATTTGA 4515
Qy      3301 TAAATATTTTCAATATCAATTTGTTCTGTTGATCTATATTAATTAATTTGAAAAA 3360
Db      4516 TAAATATTTTCAATATCAATTTGTTCTGTTGATCTATATTAATTTGAAAAA 4575
Qy      3361 TCTTTCTGAGAGAGTTCCCGAGATTTTCCAAATGAGTTCTTGGACATGACACACAG 3420
Db      4576 TCTTTCTGAGAGAGTTCCCGAGATTTTCCAAATGAGTTCTTGGACATGACACACAG 4635
Qy      3421 AGTAAAGAACTGATTTTAAAGGCTTAACTGACATTTGCTGCTGAGATGCAAGCTGAATT 3480
Db      4636 AGTAAAGAACTGATTTTAAAGGCTTAACTGACATTTGCTGCTGAGATGCAAGCTGAATT 4695
Qy      3481 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTAAGGGGGAATTCGC 3540
Db      4696 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTAAGGGGGAATTCGC 4755
Qy      3541 CGCTTCTATAGAAATGCTCTCCCTGAGAGCTGTGAGGCTGTCTTGTGTTCTGAGCTG 3600
Db      4756 CGCTTCTATAGAAATGCTCTCCCTGAGAGCTGTGAGGCTGTCTTGTGTTCTGAGCTG 4815
Qy      3601 GCTGTTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
Db      4816 GCTGTTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4875
Qy      3661 AGCATAGTCCGAGCAGAGTGAAGTTTCAATGAGTTTGCAGAGTGAATGGAATATTA 3720
Db      4876 AGCATAGTCCGAGCAGAGTGAAGTTTCAATGAGTTTGCAGAGTGAATGGAATATTA 4935
Qy      3721 ACTAGAAATATATCTTGTGTAATCAGACACAGTACTCTGTGTAAGTGTGTATC 3780
Db      4936 ACTAGAAATATATCTTGTGTAATCAGACACAGTACTCTGTGTAAGTGTGTATC 4995
Qy      3781 --GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3838
Db      4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5055
Qy      3839 GGGTATAGGATGATAAATTGGGATGTTCTTTTAAAGAAATCTCAACAGACTTCTG 3898
Db      5056 GGGTATAGGATGATAAATTGGGATGTTCTTTTAAAGAAATCTCAACAGACTTCTG 5115
Qy      3899 AAGGTATTTTCTAAGAACTTGTGCTGAGCGTGAAGCAACCCCTGTGACAGCCCC 3958
Db      5116 AAGGTATTTTCTAAGAACTTGTGCTGAGCGTGAAGCAACCCCTGTGACAGCCCC 5175
Qy      3959 ACCAGCCTGACGTGGCAGCTCTGTCTTCTCCCATGAAGAGGTGGCTCCCATATATA 4018
Db      5176 ACCAGCCTGACGTGGCAGCTCTGTCTTCTCCCATGAAGAGGTGGCTCCCATATATA 5235

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Qy      4019 TAAACCTCTCTGAGCTCAGGATGAGCAGCAAGGCCACCCATCCAGGACCTCTCAGC 4078
Db      5236 TAAACCTCTCTGAGCTCAGGATGAGCAGCAAGGCCACCCATCCAGGACCTCTCAGC 5295
Qy      4079 ACAGC 4083
Db      5296 ACAGC 5300

RESULT 8
AAVS1361
ID AAVS1361 standard; DNA; 5299 BP.
XX
XX
XX AAVS1361;
AC
AC 27-OCT-1998 (first entry)
XX
XX Human TIGR promoter region DNA.
DE
DE TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.
XX
XX Homo sapiens.
OS
OS MO9832850-A1.
PN
PN 30-JUL-1998.
XX
XX 09-JAN-1998; 98WO-US000468.
PF
PF 28-JAN-1997; 97US-00791154.
PR
PR 26-SEP-1997; 97US-00938669.
XX
XX (RBC ) UNIV CALIFORNIA.
PA
PA Nguyen TD, Polansky JR, Chen P, Chen H;
PI
PI WPI, 1998-427946/36.
XX
XX
XX Use of TIGR nucleic acid sequences - used for, e.g. developing products
PT for diagnosis, prognosis and treatment of glaucoma.
XX
XX
XX Claim 34; Fig 1; 105bp; English.
XX
XX This sequence is a trabecular meshwork induced glucocorticoid response
XX protein (TIGR) promoter region which is used in a method for diagnosing
XX glaucoma in a patient. The method involves the detection of polymorphisms
XX whose presence is predictive of a mutation affecting TIGR response in the
XX CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
XX substitutions and base additions upstream of and within TIGR exons can
XX also be used to diagnose glaucoma
XX
XX
XX Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 U; 0 Other;
SQ

Query Match 67.8%; Score 4068.4; DB 2; Length 5299;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy      1 GCTCCACAGAAAGTCTCCCACTTACGACTTCTGATCAGATGTTTACAGCCAGAAAGCTC 60
Db      1216 GCTCCACAGAAAGTCTCCCACTTACGACTTCTGATCAGATGTTTACAGCCAGAAAGCTC 1275
Qy      61 CGTGAAGGATGAGGCTGTGTCTTACACCTACCTGATAGCTCTACACCTGAGCTCACTGC 120
Db      1276 CGTGAAGGATGAGGCTGTGTCTTACACCTACCTGATAGCTCTACACCTGAGCTCACTGC 1335
Qy      121 AACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTGAGCTCCCGGTAGCTGAGACT 180
Db      1336 AACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTGAGCTCCCGGTAGCTGAGACT 1395
Qy      181 ACAGGCGACGCGCGGCTAATTTTGTATTTGATAGAGATGGGTTTACCATATTAG 240

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Db 1396 ACAGGGCACGCCCCGCTAAATTTTGTATGTTAGTAGAGATGGGGTTTCACCAATATAG 1455
Qy 241 CCCGCGTGTCTTGAATCTCCTGACCTCAGGTGATGCCACCACTCAGCTCTTAAGTGC 300
Db 1456 CCGGCGTGTCTTGAATCTCCTGACCTCAGGTGATGCCACCACTCAGCTCTTAAGTGC 1515
Qy 301 TGGGATTAACAGGATGATGACCGCGCCCGGCAAGGGTCAGTGTTTAATAGAAATAC 360
Db 1516 TGGGATTAACAGGATGATGACCGCGCCCGGCAAGGGTCAGTGTTTAATAGAAATAC 1575
Qy 361 TTGAATGTTTACTTAAACCAACAGGAAACAGACAAAGCTGTGATTAATTCAGGATTC 420
Db 1576 TTGAATGTTTACTTAAACCAACAGGAAACAGACAAAGCTGTGATTAATTCAGGATTC 1635
Qy 421 TTGGGATGGGGAATGGTGCCATGAGCTGCTGCTAGTCCAGACCACTGGTCTCATCA 480
Db 1636 TTGGGATGGGGAATGGTGCCATGAGCTGCTGCTAGTCCAGACCACTGGTCTCATCA 1695
Qy 481 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTACATTTTAATCCATGCTTTTGTG 540
Db 1696 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTACATTTTAATCCATGCTTTTGTG 1755
Qy 541 GTAAGCTCCACATCGTCTACTGAAATTAAGATTAATCAATAACTAGTTCCATTTGGGCCA 600
Db 1756 GTAAGCTCCACATCGTCTACTGAAATTAAGATTAATCAATAACTAGTTCCATTTGGGCCA 1815
Qy 601 TCTGTGTGTGTATAGGGGAGAGGGGATACCCCAAGACCTCTTGAAGCCCCCGGACG 660
Db 1816 TCTGTGTGTGTATAGGGGAGAGGGGATACCCCAAGACCTCTTGAAGCCCCCGGACG 1875
Qy 661 AGGTTTCTCTCCAGCTGGGGGAGCCCTGCAAGCACCGGGGTCCTGGGTGCTTGAGCA 720
Db 1876 AGGTTTCTCTCCAGCTGGGGGAGCCCTGCAAGCACCGGGGTCCTGGGTGCTTGAGCA 1935
Qy 721 ACTGCGACCCCGTGGCACTGCTGTTGTTTGTATCACTCTCAAGGACCTGTTGCTTCT 780
Db 1936 ACTGCGACCCCGTGGCACTGCTGTTGTTTGTATCACTCTCAAGGACCTGTTGCTTCT 1995
Qy 781 ATTTCTGTGTACTCGTTCAATTCATCAGGCAATTCATTAATTAAGATTAATTA 840
Db 1996 ATTTCTGTGTACTCGTTCAATTCATCAGGCAATTCATTAATTAAGATTAATTA 2055
Qy 841 TCTGCCAGACACCAAGACAAAATGTTGAGCAAGCACTGCTGCTTACCTTCTGAGAG 900
Db 2056 TCTGCCAGACACCAAGACAAAATGTTGAGCAAGCACTGCTGCTTACCTTCTGAGAG 2115
Qy 901 GTGACAGTTTCTCATGGAAGAAGTGCAGAAAGAAATTAATAGCAGCCCACTTAAACCA 960
Db 2116 GTGACAGTTTCTCATGGAAGAAGTGCAGAAAGAAATTAATAGCAGCCCACTTAAACCA 2175
Qy 961 GTGCTGAAGAAGAAATTAACACCATCTTGAAGAAATGTGCGAGCAATCCCTTAACA 1020
Db 2176 GTGCTGAAGAAGAAATTAACACCATCTTGAAGAAATGTGCGAGCAATCCCTTAACA 2235
Qy 1021 GGGCACTTCCCTAGCGCCCCCTGCTGCCTCATCTGTCGCCGAGGCCCCCAAGCCGAGT 1080
Db 2236 GGGCACTTCCCTAGCGCCCCCTGCTGCCTCATCTGTCGCCGAGGCCCCCAAGCCGAGT 2295
Qy 1081 CTTTCAAGGCTCTCTCTCATCATGATCAAGCGCTGAGCTGGCTGCTGCTTCCCGTG 1140
Db 2296 CTTTCAAGGCTCTCTCTCATCATGATCAAGCGCTGAGCTGGCTGCTGCTTCCCGTG 2355
Qy 1141 AATGCTCTGTGATCTTGAAGCTGAGACCTCGTTGGCTCAGGCTCCAGAAAGAAATAG 1200
Db 2356 AATGCTCTGTGATCTTGAAGCTGAGACCTCGTTGGCTCAGGCTCCAGAAAGAAATAG 2415
Qy 1201 AGAGGAAAATAGTCTTAACGAGAAATCTGAGAGGGAACAGTGTGTTCTCTAGAGGAAAGG 1260
Db 2416 AGAGGAAAATAGTCTTAACGAGAAATCTGAGAGGGAACAGTGTGTTCTCTAGAGGAAAGG 2475
Qy 1261 GCTTCAAGCTCCAGAGAAATTCAGAGAGGTGGGACTGCAAGAGAGTGGGGAACGCTGGGGC 1320
Db 2476 GCTTCAAGCTCCAGAGAAATTCAGAGAGGTGGGACTGCAAGAGAGTGGGGAACGCTGGGGC 2535

Qy 1321 TGAGCGGAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
Db 2536 TGAGCGGAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2595
Qy 1381 AGTGTGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
Db 2596 AGTGTGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2655
Qy 1441 CTGCTTGAAGAGAGAAAGTCTATTTTCAATGAAGGATGCAAGTTTCATTAAGTCACTGTT 1500
Db 2656 CTGCTTGAAGAGAGAAAGTCTATTTTCAATGAAGGATGCAAGTTTCATTAAGTCACTGTT 2715
Qy 1501 AAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Db 2716 AAAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2775
Qy 1561 GAAGCAGCTCATTTCTTAAGGCGGTAATTAACGGAAGAGTGAAGTGAAGTCTTTCTTT 1620
Db 2776 GAAGCAGCTCATTTCTTAAGGCGGTAATTAACGGAAGAGTGAAGTGAAGTCTTTCTTT 2835
Qy 1621 CATGCTTTCTGGGCACTACTAGCCCTGTGTGAAGCTTGGCTTATGCAAGCGTCCAA 1680
Db 2836 CATGCTTTCTGGGCACTACTAGCCCTGTGTGAAGCTTGGCTTATGCAAGCGTCCAA 2895
Qy 1681 AACCTTGAATCAGAGAGCTGGGTTTCTTCTGTTCTGCAATGGTTGGCTGTGCGAC 1740
Db 2896 AACCTTGAATCAGAGAGCTGGGTTTCTTCTGTTCTGCAATGGTTGGCTGTGCGAC 2955
Qy 1741 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCTTAAGAACCTTTGCA 1800
Db 2956 CGTGGGCAAGTGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCTTAAGAACCTTTGCA 3015
Qy 1801 GCTCTGTGTGTGTGAACACTTCCCTGTGATTTCTGTGAGGGGGAGTGTGAAGGGG 1860
Db 3016 GCTCTGTGTGTGTGAACACTTCCCTGTGATTTCTGTGAGGGGGAGTGTGAAGGGG 3075
Qy 1861 AAGGAGGAGAGAGCTGAGAGAGCTGAGCCACAGGGAGGTGAGGGGAGACAGAAAGCAG 1920
Db 3076 AAGGAGGAGAGAGCTGAGAGAGCTGAGCCACAGGGAGGTGAGGGGAGACAGAAAGCAG 3135
Qy 1921 CAGAACTGGGTGCTCCATCAGTCTCATCTGATCACTGATCACTGATCACTGATCACTG 1980
Db 3136 CAGAACTGGGTGCTCCATCAGTCTCATCTGATCACTGATCACTGATCACTGATCACTG 3195
Qy 1981 CAATGCTTCAAGAAAGTCAATGAACCAACAGCCCAATTTTCTTCCCTAAGCATAGAC 2040
Db 3196 CAATGCTTCAAGAAAGTCAATGAACCAACAGCCCAATTTTCTTCCCTAAGCATAGAC 3255
Qy 2041 AATGGCAATTTGCCAATTAACCAAAAGAAATGCAAGACCTTAAGTGTGTTGCTG 2100
Db 3256 AATGGCAATTTGCCAATTAACCAAAAGAAATGCAAGACCTTAAGTGTGTTGCTG 3315
Qy 2101 GCATTCAAAACCTGGGCGAGAGCAAGTGAAGAAATGCCAGAGATGTGTTAACTTTTCA 2160
Db 3316 GCATTCAAAACCTGGGCGAGAGCAAGTGAAGAAATGCCAGAGATGTGTTAACTTTTCA 3375
Qy 2161 TGAACAGACCCCGACGAGCTCAGCACTGCTGACAGCAAGGAGTGAAGCTGACGCGC 2220
Db 3376 TGAACAGACCCCGACGAGCTCAGCACTGCTGACAGCAAGGAGTGAAGCTGACGCGC 3435
Qy 2221 AGGGAGAGAGAAAGAAAGAGAGGAGTGTATAGAGAAAGAAAGACAGATTCAATTCAG 2280
Db 3436 AGGGAGAGAGAAAGAAAGAGAGGAGTGTATAGAGAAAGAAAGACAGATTCAATTCAG 3495
Qy 2281 GGCAGTGGAAATTGACACAGGGAATTATAGTCCAGTATCTGGGTTCTAGAGAGCAGG 2340
Db 3496 GGCAGTGGAAATTGACACAGGGAATTATAGTCCAGTATCTGGGTTCTAGAGAGCAGG 3555
Qy 2341 GCTATATTTGTGGGGGAAAAAATCAAGTTCAAGGGAAGTGGGAGACCTGATTTCTAATAC 2400
Db 3556 GCTATATTTGTGGGGGAAAAAATCAAGTTCAAGGGAAGTGGGAGACCTGATTTCTAATAC 3615

QY	2401	TATATTTTCCCTTACAAAGCTAGATAATTCGAGCAAGTCAACAAGTAGTACAGAGCT	2460
Dp	3616	TATATTTTCCCTTACAAAGCTAGATAATTCGAGCAAGTCAACAAGTAGTACAGAGCT	3675
QY	2461	GTAAGATTACTACTTCTCTCTTATTAAGAACTCTTTTCTCTGTGAGTTAGACAGACA	2520
Dp	3676	GTAAGATTACTACTTCTCTCTTATTAAGAACTCTTTTCTCTGTGAGTTAGACAGACA	3735
QY	2521	AGGGCAATCCCGTTTCTTTTACAGGAAGAAACATTCTTAAGTAAAGCCAAACAGAT	2580
Dp	3736	AGGGCAATCCCGTTTCTTTTACAGGAAGAAACATTCTTAAGTAAAGCCAAACAGAT	3795
QY	2581	TCAAGCCATGAGCTTGTGCACTATATATATGGTTTTTGGAAAAATCATTTCAAGCATGT	2640
Dp	3796	TCAAGCCATGAGCTTGTGCACTATATATATGGTTTTTGGAAAAATCATTTCAAGCATGT	3855
QY	2641	TACTATCTGATTCAAGAAATATAGACTAGTACCCTTGGTCAAGCTGTAAACAAACCCAT	2700
Dp	3856	TACTATCTGATTCAAGAAATATAGACTAGTACCCTTGGTCAAGCTGTAAACAAACCCAT	3915
QY	2701	TTGTAAATGTCTCAAGTTCAAGCTTAACTGCAAGCAACATCAATTAAGATAGATCTTT	2760
Dp	3916	TTGTAAATGTCTCAAGTTCAAGCTTAACTGCAAGCAACATCAATTAAGATAGATCTTT	3975
QY	2761	AGAGCAAACTGTGTTTCTCCCACTCTGAGAGTGAATCTGCCAGAGGCACTTGGAAATTTT	2820
Dp	3976	AGAGCAAACTGTGTTTCTCCCACTCTGAGAGTGAATCTGCCAGAGGCACTTGGAAATTTT	4035
QY	2821	ACTTCACAAAGATTGACACACTGTGTGGTATTAACAATTAAGTTGCTCAAGGCAATC	2880
Dp	4036	ACTTCACAAAGATTGACACACTGTGTGGTATTAACAATTAAGTTGCTCAAGGCAATC	4095
QY	2881	ATTATTTCAAGTGGCTTAAAGTTACTTCGACAGTTTGTATATTTATGGCTATTTGCC	2940
Dp	4096	ATTATTTCAAGTGGCTTAAAGTTACTTCGACAGTTTGTATATTTATGGCTATTTGCC	4155
QY	2941	ATTTGCTTTTGTGTTTTTCTCTTTGGGTTATTTAATGTAAGACAGGATTTATTAACCTAC	3000
Dp	4156	ATTTGCTTTTGTGTTTTTCTCTTTGGGTTATTTAATGTAAGACAGGATTTATTAACCTAC	4215
QY	3001	AGTCGAGAAACCTGTGTAATTTGATGAGAAAAATTACATTTTGTGTTTACACCTT	3060
Dp	4216	AGTCGAGAAACCTGTGTAATTTGATGAGAAAAATTACATTTTGTGTTTACACCTT	4275
QY	3061	CTAACTAAATTTAAACATTTTATTCATTTCCGATATAGAGCCATTAACCTCAAGTGTATAT	3120
Dp	4276	CTAACTAAATTTAAACATTTTATTCATTTCCGATATAGAGCCATTAACCTCAAGTGTATAT	4335
QY	3121	ACAGTACTCTGTGATTTTGTCAATTACCAATAGAAATCACAGACATTTTATCTATATTACA	3180
Dp	4336	ACAGTACTCTGTGATTTTGTCAATTACCAATAGAAATCACAGACATTTTATCTATATTACA	4395
QY	3181	GTTGTGTCAGADPAGGTGTGAAGTGAATAATTATATCTCAAAACATCTTGAATTTAGACC	3240
Dp	4396	GTTGTGTCAGADPAGGTGTGAAGTGAATAATTATATCTCAAAACATCTTGAATTTAGACC	4455
QY	3241	TCCTGCTGATCTGTGTTTTTAAACATTAATTAATAACATGTTTAAATTTGATATTTTGA	3300
Dp	4456	TCCTGCTGATCTGTGTTTTTAAACATTAATTAATAACATGTTTAAATTTGATATTTTGA	4515
QY	3301	TAAATCAATTTTCATTAATCAATTTGTTCTTTGTGAATCTATATATTTATTTGAAAACA	3360
Dp	4516	TAAATCAATTTTCATTAATCAATTTGTTCTTTGTGAATCTATATATTTATTTGAAAACA	4575
QY	3361	TCTTTCTGAGAAAGTTCCCAAGATTTTACCAATGAAGGTTCTTGACATGCAACAACAG	3420
Dp	4576	TCTTTCTGAGAAAGTTCCCAAGATTTTACCAATGAAGGTTCTTGACATGCAACAACAG	4635
QY	3421	AGTAAGAATGATTTAGAGGCTAAACATTTGATGGTCTGAGATGCAACAATCTGAAAT	3480
Dp	4636	AGTAAGAATGATTTAGAGGCTAAACATTTGATGGTCTGAGATGCAACAATCTGAAAT	4695
QY	3481	AGAAAGTTCTCCCAAGATACACAGTTGTTTTTAAAGCTAAGGGGTGAGGGGGAATCTGC	3540

[illegible]

XX (REGC) UNIV CALIFORNIA.
 XX Nguyen TD, Polansky JR, Chen P, Chen H;
 XX WPI; 1998-427946/36.
 DR
 XX
 XX Use of TIGR nucleic acid sequences - used for, e.g. developing products
 PT for diagnosis, prognosis and treatment of glaucoma.
 XX
 XX
 PS Disclosure; Fig 2; 105dp; English.
 CC This sequence is a trabecular meshwork induced glucocorticoid response
 CC protein (TIGR) promoter mutant, TIGRm4, which is used in a method for
 CC diagnosing glaucoma in a patient. The method involves the detection of
 CC polymorphisms whose presence is predictive of a mutation affecting TIGR
 CC response in the patient and can be diagnostic of glaucoma or steroid
 CC sensitivity. Base substitutions and base additions upstream of and within
 CC TIGR exons can also be used to diagnose glaucoma
 XX
 XX
 SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 U; 0 Other;
 Query Match 67.8%; Score 4067.8; DB 2; Length 5300;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
 QY 1 GCTCCAGAGAACTCTCCCACTCTGAGACTTCTGATCCAGATTTACAGCCAGAAAGCTC 60
 DB 1216 GCTCCAGAGAACTCTCCCACTCTGAGACTTCTGATCCAGATTTACAGCCAGAAAGCTC 1275
 QY 61 CGTAGAGGTGAGGGTCTGTGCTTTACACCTACCTGATGCTCTACACCTGAGCTCACTGC 120
 DB 1276 CGTAGAGGTGAGGGTCTGTGCTTTACACCTACCTGATGCTCTACACCTGAGCTCACTGC 1335
 QY 121 AACCTCTGCTCCAGAGTTACAGCAATCTCTGCTCAGCCTCCGCGTGAAGTGGAGCT 180
 DB 1336 AACCTCTGCTCCAGAGTTACAGCAATCTCTGCTCAGCCTCCGCGTGAAGTGGAGCT 1395
 QY 181 ACAGGGCAGCGCCGGCTAATTTTGTATTTAGTATGAGATGGGGTTTACCATTTAG 240
 DB 1396 ACAGGGCAGCGCCGGCTAATTTTGTATTTAGTATGAGATGGGGTTTACCATTTAG 1455
 QY 241 CCCGGCTGATCTTGAATCTCTGACTCAGGTGATCCACCACCTCAGCCTCTTAAAGTGC 300
 DB 1456 CCCGGCTGATCTTGAATCTCTGACTCAGGTGATCCACCACCTCAGCCTCTTAAAGTGC 1515
 QY 301 TGGGATTAACAGGATGATGATCCGCGCCCGGCGCAAGGGTCAAGTGTATTAATAGGAATAC 360
 DB 1516 TGGGATTAACAGGATGATGATCCGCGCCCGGCGCAAGGGTCAAGTGTATTAATAGGAATAC 1575
 QY 361 TTGAATGTTTACTAACAACAGGGAACAGACAAAGCTGATGATTAATTTTCAAGGATTC 420
 DB 1576 TTGAATGTTTACTAACAACAGGGAACAGACAAAGCTGATGATTAATTTTCAAGGATTC 1635
 QY 421 TTGGGATGGGGAATGGTGCATGAGCTGCTGCTGATCCAGAACCACTGATGCTCATCA 480
 DB 1636 TTGGGATGGGGAATGGTGCATGAGCTGCTGCTGATCCAGAACCACTGATGCTCATCA 1695
 QY 481 CTTTCTTCCCTCATCTCATATTTTCAAGGCTAAGTTACATTTTATTCACCATGCTTTTGG 540
 DB 1696 CTTTCTTCCCTCATCTCATATTTTCAAGGCTAAGTTACATTTTATTCACCATGCTTTTGG 1755
 QY 541 GTTAGGCTCCACATGTTTCTGAAATTAAGATTAACATTAACATGTTTCAATTTTGGGCGCA 600
 DB 1756 GTTAGGCTCCACATGTTTCTGAAATTAAGATTAACATTAACATGTTTCAATTTTGGGCGCA 1815
 QY 601 TCTGTGTGTGTATTAAGGGAAGGAGGATACCCCAAGAGACTCTTGAAGCCCGGCGAG 660
 DB 1816 TCTGTGTGTGTATTAAGGGAAGGAGGATACCCCAAGAGACTCTTGAAGCCCGGCGAG 1875
 QY 661 AAGTTTCTCTCAAGTGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTGTCTGAGCA 720
 DB 1876 AAGTTTCTCTCAAGTGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTGTCTGAGCA 1935

QY 721 ACCGCGAGCCGCTGACAGTGGTGTGTTTATTCATCTGCTTAGGAGCCGTTGCTTCT 780
 DB 1936 ACCGCGAGCCGCTGACAGTGGTGTGTTTATTCATCTGCTTAGGAGCCGTTGCTTCT 1995
 QY 781 ATTCTGTGTGACTCGTTTCAATTCATCCAGGCAATTCATTAATTAATTAATTAATTA 840
 DB 1996 ATTCTGTGTGACTCGTTTCAATTCATCCAGGCAATTCATTAATTAATTAATTAATTA 2055
 QY 841 TCTGCCAGACACCAAGACAAATGTTGACCAAGCATCTGCTTACCTTCTGAGAG 900
 DB 2056 TCTGCCAGACACCAAGACAAATGTTGACCAAGCATCTGCTTACCTTCTGAGAG 2115
 QY 901 GTGACAGTTTTCATGAGGAAGGTGAGGAAGAAATTAATTAATTAATTAATTAATTA 960
 DB 2116 GTGACAGTTTTCATGAGGAAGGTGAGGAAGAAATTAATTAATTAATTAATTAATTA 2175
 QY 961 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGCAGCATTCCTTAACA 1020
 DB 2176 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGCAGCATTCCTTAACA 2235
 QY 1021 GGCACCTCTCTAGCGCCCTGCTGCTCCATCTGTCGCCGAGGCCCAAGCCGAGT 1080
 DB 2236 GGCACCTCTCTAGCGCCCTGCTGCTCCATCTGTCGCCGAGGCCCAAGCCGAGT 2295
 QY 1081 CTTCCAGGCTCTCTCTCATCATGATCAGCGCTGAGCTGAGCTTCTGCTTCCCGTG 1140
 DB 2296 CTTCCAGGCTCTCTCTCATCATGATCAGCGCTGAGCTGAGCTTCTGCTTCCCGTG 2355
 QY 1141 AATCGCTCTGTGATCTTGAAGTGAAGACTCTTGGCTCAGAGCTCAGAAAGAAATAG 1200
 DB 2356 AATCGCTCTGTGATCTTGAAGTGAAGACTCTTGGCTCAGAGCTCAGAAAGAAATAG 2415
 QY 1201 AAGAGAAATCTAGCTTAACGAGAAATCTGAGAGGGAACAAGTCTTCTCAGAGAAAGG 1260
 DB 2416 AAGAGAAATCTAGCTTAACGAGAAATCTGAGAGGGAACAAGTCTTCTCAGAGAAAGG 2475
 QY 1261 GCTCCAGGTCAGAGAAATTCAGAGAGTGGGGCTGCAAGGAGTGGGGAAGCTGGGGC 1320
 DB 2476 GCTCCAGGTCAGAGAAATTCAGAGAGTGGGGCTGCAAGGAGTGGGGAAGCTGGGGC 2535
 QY 1321 TGAAGCGGTGCTGAAGAGGAGGAGAAAGGCAAGGCTGAAGCTCCAGATGTC 1380
 DB 2536 TGAAGCGGTGCTGAAGAGGAGGAGAAAGGCAAGGCTGAAGCTCCAGATGTC 2595
 QY 1381 AGTGTGTTTCAAGGAGCTGGAGGTTTCTGTTGCTTCTGAGGCTTTTATCTTTTCT 1440
 DB 2596 AGTGTGTTTCAAGGAGCTGGAGGTTTCTGTTGCTTCTGAGGCTTTTATCTTTTCT 2655
 QY 1441 CTGCTTGAAGAGAAAGAGTCTAATTCATGAAGGATGCAATTTTCAATTAAGTCACTGTT 1500
 DB 2656 CTGCTTGAAGAGAAAGAGTCTAATTCATGAAGGATGCAATTTTCAATTAAGTCACTGTT 2715
 QY 1501 AAAATTTCCAGGAGTGAATGGGTTTCTCTCAAGAGGCTTTATTAATGGAATATAG 1560
 DB 2716 AAAATTTCCAGGAGTGAATGGGTTTCTCTCAAGAGGCTTTATTAATGGAATATAG 2775
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 DB 2836 CATGTCTTCTGGGCAACTACTACGCTGCTGTGAGCACTTGCTTATTCAGACGGTCCGA 2895
 QY 1681 AACCTTGAATCAGAGACTCGGTTTCTTCTGAGTTCTGCAATGTTGGCTGAGC 1740
 DB 2896 AACCTTGAATCAGAGACTCGGTTTCTTCTGAGTTCTGCAATGTTGGCTGAGC 2955
 QY 1741 CGTGGGCAAGTGTCTCTCTTCTGAGCCATAGTCTTCTGCTAATAAGACCTTGC 1800
 DB 2956 CGTGGGCAAGTGTCTCTCTTCTGAGCCATAGTCTTCTGCTAATAAGACCTTGC 3015

QY 1801 GCTCTGTTCTGTGACACCTCCCTGTGATCTCTGTGAGGGGGAGTGTGAGAGGG 1860
 Db 3016 GCTCTGTTCTGTGACACCTCCCTGTGATCTCTGTGAGGGGGAGTGTGAGAGGG 3075
 QY 1861 AAGAGGCAAGCTGTGAGAGCTGAGCCACAGGGAGGTGAGGGGACAGAAAGGCAG 1920
 Db 3076 AAGAGGCAAGCTGTGAGAGCTGAGCCACAGGGAGGTGAGGGGACAGAAAGGCAG 3135
 QY 1921 CAGAAAGCTGGGTCCATCATGCTCTCATATCATCGTCAGACTCCAGAGCCGAGGCCA 1980
 Db 3136 CAGAAAGCTGGGTCCATCATGCTCTCATATCATCGTCAGAGCTCCAGAGCCGAGGCCA 3195
 QY 1981 CAATGCTTCAGAAAAGCTCAATGAAACCCACAGCCACATTTTCTTCCCTAAGCATAGAC 2040
 Db 3196 CAATGCTTCAGAAAAGCTCAATGAAACCCACAGCCACATTTTCTTCCCTAAGCATAGAC 3255
 QY 2041 AATGGCATTTGGCAATTAACCAAAAAGAAATGCAAGAGCTAATCTGGTGTAGCTTTGCTG 2100
 Db 3256 AATGGCATTTGGCAATTAACCAAAAAGAAATGCAAGAGCTAATCTGGTGTAGCTTTGCTG 3315
 QY 2101 GCATTCAAAACCTGGGCCAGAGCAAGTGGAAAATGCGCAGAGATTTGTAACTTTTCAACC 2160
 Db 3316 GCATTCAAAACCTGGGCCAGAGCAAGTGGAAAATGCGCAGAGATTTGTAACTTTTCAACC 3375
 QY 2161 TGACCAAGACCCCAAGCAGCTCAGCAGTGAAGTGTGACAGCAGAGTGAACCTGAGAGGC 2220
 Db 3376 TGACCAAGACCCCAAGCAGCTCAGCAGTGAAGTGTGACAGCAGAGTGAACCTGAGAGGC 3435
 QY 2221 AAGGGAGAGAAAGAAAAGAGAGGATGTGTATGAGCAAGAAAGACAGATTCATTCAAG 2280
 Db 3436 AAGGGAGAGAAAGAAAAGAGAGGATGTGTATGAGCAAGAAAGACAGATTCATTCAAG 3495
 QY 2281 GGCAGTGGGAATTTGACACAGGATTTATAGTCACATGATCTGTGGTTCTAGAGAGCAG 2340
 Db 3496 GGCAGTGGGAATTTGACACAGGATTTATAGTCACATGATCTGTGGTTCTAGAGAGCAG 3555
 QY 2341 GCTATATTTGTGGGGGAAAAAATACAGTTCAAGGAAGTCGGAGACCTGATTTCTAATAC 2400
 Db 3556 GCTATATTTGTGGGGGAAAAAATACAGTTCAAGGAAGTCGGAGACCTGATTTCTAATAC 3615
 QY 2401 TATATTTTTCTTTTCAAGCTGATTAATTTCTGAGCAAGTCACAGATGTAACTGAGCT 2460
 Db 3616 TATATTTTTCTTTTCAAGCTGATTAATTTCTGAGCAAGTCACAGATGTAACTGAGCT 3675
 QY 2461 GTPAATATCTAGATTTCTCCTTATAGGAATCTTTTCTCTGTGAGATTAGCAGACA 2520
 Db 3676 GTPAATATCTAGATTTCTCCTTATAGGAATCTTTTCTCTGTGAGATTAGCAGACA 3735
 QY 2521 AAGGCAATCCCGTTCTTTTAAACAGAAAGAAAACATTCCTAAGATTAAGCCAAACAGAT 2580
 Db 3736 AAGGCAATCCCGTTCTTTTAAACAGAAAGAAAACATTCCTAAGATTAAGCCAAACAGAT 3795
 QY 2581 TCAAGCCTTAGTCTTGTCTGATCTATATGATGTGTTTTTGAATAATCATTTCAAGATGT 2640
 Db 3796 TCAAGCCTTAGTCTTGTCTGATCTATATGATGTGTTTTTGAATAATCATTTCAAGATGT 3855
 QY 2641 TACTATCTGATTCAGAAAATGAGACTAGTAAACCTTTGTGCTGAGCTGTAACAAACCCAT 2700
 Db 3856 TACTATCTGATTCAGAAAATGAGACTAGTAAACCTTTGTGCTGAGCTGTAACAAACCCAT 3915
 QY 2701 TTGTAATGTCTCAAGTTAGGCTTAATCTGAGAAACCAATCAAAATGAATGAATCTTT 2760
 Db 3916 TTGTAATGTCTCAAGTTAGGCTTAATCTGAGAAACCAATCAAAATGAATGAATCTTT 3975
 QY 2761 AAGAGCAATCTGTGTTTCTCACTCTGAGAGTGAAGTCTGCAAGGCAAGTTTGAATATTT 2820
 Db 3976 AAGAGCAATCTGTGTTTCTCACTCTGAGAGTGAAGTCTGCAAGGCAAGTTTGAATATTT 4035
 QY 2821 ACTTCAAGATTTGACAGCTGTTGTGTATTAACAACAATAAGTTGCTCAAGGCAATC 2880
 Db 4036 ACTTCAAGATTTGACAGCTGTTGTGTATTAACAACAATAAGTTGCTCAAGGCAATC 4095
 QY 2881 ATTATTTCAAGTGGCTTAAGTACTTCTGACAGTTTGTGTATATTTATTTGCTATTTGCC 2940

Db 4096 ATTATTTCAAGTGGCTTAAGTACTTCTGACAGTTTGTGTATATTTATTTGCTATTTGCC 4155
 QY 2941 ATTGCTTTTGTGTTTTTCTTTGGGTTTATTAATGTAAGCAGGATTTATTAACCTAC 3000
 Db 4156 ATTTGCTTTTGTGTTTTTCTTTGGGTTTATTAATGTAAGCAGGATTTATTAACCTAC 4215
 QY 3001 AGTCAGAAAAGCCTGTGAATTTGAATGAGAAAATAATTAAGATTTTGTGTTTACCACTT 3060
 Db 4216 AGTCAGAAAAGCCTGTGAATTTGAATGAGAAAATAATTAAGATTTTGTGTTTACCACTT 4275
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 Db 4276 CTAACTAATTTTAACTTTTATTTCCATTGGGAATGAGCCATAACTCAAAAGTGTATA 4335
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 Db 4336 ACAGTACCTGTGATTTTGTCAATTCACAAATGAATCAAGACATTTATATATATTACA 4395
 QY 3181 GTTGTGCAAGTACGTTGTGAAGTAAATTTATATCTCAAAACTACTTTGAATTAAGACC 3240
 Db 4396 GTTGTGCAAGTACGTTGTGAAGTAAATTTATATCTCAAAACTACTTTGAATTAAGACC 4455
 QY 3241 TCTGTCTGAGATCTTGTGTTTTTAACTATTAATTAACATGTTTAAATTTTGAATTTTGA 3300
 Db 4456 TCTGTCTGAGATCTTGTGTTTTTAACTATTAATTAACATGTTTAAATTTTGAATTTTGA 4515
 QY 3301 TTAATCATTTTTCATTAATCATTTGTTTCTTTGTAATCTAATTTTATATATTGAAAAACA 3360
 Db 4516 TTAATCATTTTTCATTAATCATTTGTTTCTTTGTAATCTAATTTTATATATTGAAAAACA 4575
 QY 3361 TCTTTCTGAGAAAGATTTCCCAAGATTTCAACCAATGAAGTTCTTGGACATGACACACAG 3420
 Db 4576 TCTTTCTGAGAAAGATTTCCCAAGATTTCAACCAATGAAGTTCTTGGACATGACACACAG 4635
 QY 3421 AGTAAGAACTGATTTTAAAGGCTAACATTGACATTTGGTCCGTGAATGCCAAGACTGAATT 3480
 Db 4636 AGTAAGAACTGATTTTAAAGGCTAACATTGACATTTGGTCCGTGAATGCCAAGAATT 4695
 QY 3481 AGAAAGTTCCTCCAAAGATACACAGTTGTTTAAAGCTAGGGGTGAAGGGGAAATCTGC 3540
 Db 4696 AGAAAGTTCCTCCAAAGATACACAGTTGTTTAAAGCTAGGGGTGAAGGGGAAATCTGC 4755
 QY 3541 CGCTTCTATAGGAATGCTCTCCCTGAGCCTGTAGAGGTGCTGTCCTTGTGTTCTGCTG 3600
 Db 4756 CGCTTCTATAGGAATGCTCTCCCTGAGCCTGTAGAGGTGCTGTCCTTGTGTTCTGCTG 4815
 QY 3601 GCTGTATTTTTTCTGTCTCCTGCTAGCTTTAAAGCACTGTTTGCATCTCCAGTTCTCT 3660
 Db 4816 GCTGTATTTTTTCTGTCTCCTGCTAGCTTTAAAGCACTGTTTGCATCTCCAGTTCTCT 4875
 QY 3661 AGCATAGGCTGTGAGACAGTGCAGAGTTCTCAATGAGTTTGCAGAGTGAATGGAATATTA 3720
 Db 4876 AGCATAGGCTGTGAGACAGTGCAGAGTTCTCAATGAGTTTGCAGAGTGAATGGAATATTA 4935
 QY 3721 ACTAGAATATATCTCTGTTGTAATCAGACACAGCATAGTCTGTGTATGATGTGTATC 3780
 Db 4936 ACTAGAATATATCTCTGTTGTAATCAGACACAGCATAGTCTGTGTATGATGTGTATC 4995
 QY 3781 --GT 3838
 Db 4996 GT 5055
 QY 3839 GGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCAAAAGACATTTCTGG 3898
 Db 5056 GGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCAAAAGACATTTCTGG 5115
 QY 3899 AAGGTTATTTTCTAAGATCTTGTCTGCAAGGTGAAGGCAACCCCTGTGTGACAGCCCC 3958
 Db 5116 AAGGTTATTTTCTAAGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5175
 QY 3959 ACCGAGCTCAAGTGGCACTGTGTTTCCCAATGAAGGCTGGCTCCCAAGTATTA 4018

Db 5176 ACCGAGCTCACTGCGCACCCTGTCTTCCCTCCAGTAAGGGCTGGCTCCCACTATATA 5235
 QY 4019 TAACTCTCTGAGCTCAAGCATGAGCAGCAAGCCCATTCAGGACCTCTGAGC 4078
 Db 5236 TAAACCTCTCTGAGCTCGGGCATGAGCAGCAAGCCCATTCAGGACCTCTGAGC 5295
 QY 4079 ACAGC 4083
 Db 5296 ACAGC 5300

RESULT 10
 AAV51367
 ID AAV51367 standard; DNA; 5300 BP.
 XX
 AC AAV51367;
 XX
 DT 27-OCT-1998 (first entry)
 XX
 DE Human TIGR promoter variant TIGRv1 DNA.
 XX
 KM TIGR; trabecular meshwork induced glucocorticoid response protein; human;
 KW diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT mutation 4406
 FT /tag= a
 FT /note= "Wild-type A is replaced by G"
 XX
 PN W09832850-A1.
 XX
 PD 30-JUL-1998.
 XX
 PF 09-JAN-1998; 98WO-US000468.
 XX
 PR 28-JAN-1997; 97US-00791154.
 PR 26-SEP-1997; 97US-00938669.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Nguyen TD, Polansky JR, Chen F, Chen H;
 DR MPI; 1998-427946/36.
 XX
 PT Use of TIGR nucleic acid sequences - used for, e.g. developing products
 PT for diagnosis, prognosis and treatment of glaucoma.
 PS
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 XX
 CC This sequence is a trabecular meshwork induced glucocorticoid response
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 SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 U; 0 Other;

Query Match 67.8%; Score 4067.8; DB 2; Length 5300;
 Best local Similarity 99.9%; Pred. No. 0;
 Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 GCTCCACAGAACTCTCCCACTCTAGACTTTCGATCAAGATGTTACAGCCAGAAGCTC 60
 Db 1216 GCTCCACAGAACTCTCCCACTCTAGACTTTCGATCAAGATGTTACAGCCAGAAGCTC 1275
 QY 61 CCGAGAGGTGAGAGGTCTGTGTCTTACACCTGATATGCTTACACCTGAGCTCACTGC 120
 Db 1276 CCGAGAGGTGAGAGGTCTGTGTCTTACACCTGATATGCTTACACCTGAGCTCACTGC 1335

QY 121 AACCTGAGCCTCCAGAGTTCAAGCAATTCTCCGTCTCAAGCCTCCGGGTAAGTGGAGCT 180
 Db 1336 AACCTGAGCCTCCAGAGTTCAAGCAATTCTCCGTCTCAAGCCTCCGGGTAAGTGGAGCT 1395
 QY 181 ACAGGCGCAGCCCGGCTAATTTTGTATTTAGTAGAGATGGGTTTCAACCATTTAG 240
 Db 1396 ACAGGCGCAGCCCGGCTAATTTTGTATTTAGTAGAGATGGGTTTCAACCATTTAG 1455
 QY 241 CCGGCTGGTCTTGAACCTCTGACCTCAAGTGATCCACCACCTCAAGCTCTTAAAGTGC 300
 Db 1456 CCGGCTGGTCTTGAACCTCTGACCTCAAGTGATCCACCACCTCAAGCTCTTAAAGTGC 1515
 QY 301 TGGATTACAGGATAGTCAACCGGCGCGGCAAGGGTCAAGTTTAAATGAAGTAAC 360
 Db 1516 TGGATTACAGGATAGTCAACCGGCGCGGCAAGGGTCAAGTTTAAATGAAGTAAC 1575
 QY 361 TTGAATGTTTACTAAACCAACAGGAGAAACAGCAAAAGCTGTATTAATTCAGGATTC 420
 Db 1576 TTGAATGTTTACTAAACCAACAGGAGAAACAGCAAAAGCTGTATTAATTCAGGATTC 1635
 QY 421 TTGGATGGGGAATGTGTGCAATGAGCTGCTGTATGTCACAGCACTGTGTCTCATCA 480
 Db 1636 TTGGATGGGGAATGTGTGCAATGAGCTGCTGTATGTCACAGCACTGTGTCTCATCA 1695
 QY 481 CTTTCTCCCTCATCTCTCATTTTTCAGGGCTAAGTTACATTTTATTCACATGCTTTTGTG 540
 Db 1696 CTTTCTCCCTCATCTCTCATTTTTCAGGGCTAAGTTACATTTTATTCACATGCTTTTGTG 1755
 QY 541 GTAAGCCTCAGATCGTTACTGAATAATGAAGTATACATTAAGTATTCATTGGGGCCA 600
 Db 1756 GTAAGCCTCAGATCGTTACTGAATAATGAAGTATACATTAAGTATTCATTGGGGCCA 1815
 QY 601 TCTGTGTGTGTATAGGGAGAGGGCATACCCAGAGACTCTTGAAGCCCGGCGAG 660
 Db 1816 TCTGTGTGTGTATAGGGAGAGGGCATACCCAGAGACTCTTGAAGCCCGGCGAG 1875
 QY 661 AGGTTTCCCTCAGCTGGGGAGGCCCTGCAAGCACCCGGGCTCTGGGTGTCCTGAGCA 720
 Db 1876 AGGTTTCCCTCAGCTGGGGAGGCCCTGCAAGCACCCGGGCTCTGGGTGTCCTGAGCA 1935
 QY 721 ACCTGCAGCCCGTGCACACTGTGTGTTTGTATCACTCTTGAAGGACCTGTGCTTCT 780
 Db 1936 ACCTGCAGCCCGTGCACACTGTGTGTTTGTATCACTCTTGAAGGACCTGTGCTTCT 1995
 QY 781 ATTTCTGTGTGACTCGTTCAATTCATTCAGGACATTCATGAACAATTTATGAGTACTATA 840
 Db 1996 ATTTCTGTGTGACTCGTTCAATTCATTCAGGACATTCATGAACAATTTATGAGTACTATA 2055
 QY 841 TCTGCCAGCACCAAGACAAATATGTGAGCAAAAGCATGCTGCCCTTACCTTGTGAG 900
 Db 2056 TCTGCCAGCACCAAGACAAATATGTGAGCAAAAGCATGCTGCCCTTACCTTGTGAG 2115
 QY 901 GTGACAGTTTCTCATGAAAGCGTCAGAGAAATTAATATAGCCAGCAATTAACCCA 960
 Db 2116 GTGACAGTTTCTCATGAAAGCGTCAGAGAAATTAATATAGCCAGCAATTAACCCA 2175
 QY 961 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGAAATTTGCGAGCATCTCTTAACA 1020
 Db 2176 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGAAATTTGCGAGCATCTCTTAACA 2235
 QY 1021 GGGCACTCCCTAGAGGCCCCCGTGCCTCAATGTCGCCGAGAGCCCAAGCCCGAGT 1080
 Db 2236 GGGCACTCCCTAGAGGCCCCCGTGCCTCAATGTCGCCGAGAGCCCAAGCCCGAGT 2295
 QY 1081 CTTCCAGGCTCTCTCTCATAGTCAAGAGCTGCACTGGCTGCTGCTTCCCGT 1140
 Db 2296 CTTCCAGGCTCTCTCTCATAGTCAAGAGCTGCACTGGCTGCTGCTTCCCGT 2355
 QY 1141 AATGCTCTGTGTGATCTGAGCTGAGACTCTTGTGCTCAGAGCTCAGAAAGAAATGG 1200
 Db 2356 AATGCTCTGTGTGATCTGAGCTGAGACTCTTGTGCTCAGAGCTCAGAAAGAAATGG 2415

QY	1201	AGAGGAAAAC	TAGTCTAA	CGAGAAATCT	GGAGGGGACAGTGTTCCT	CAAGGGAAAGG	1260
Db	2416	AGAGGAAAAC	TAGTCTAA	CGAGAAATCT	GGAGGGGACAGTGTTCCT	CAAGGGAAAGG	2475
QY	1261	GCCTCACG	CTCAGAGAAATTC	CAAGAGGTGGGAC	CTGCAGAGGAGTGGGACGCTGGAGG	1320	
Db	2476	GCCTCACG	CTCAGAGAAATTC	CAAGAGGTGGGAC	CTGCAGAGGAGTGGGACGCTGGAGG	2535	
QY	1321	TGAGCGG	TGCTGAAGG	CCAGAGAGGTGA	AAAAAGGCGACAGCTGAAGCTGCCAGATGTC	1380	
Db	2536	TGAGCGG	TGCTGAAGG	CCAGAGAGGTGA	AAAAAGGCGACAGCTGAAGCTGCCAGATGTC	2595	
QY	1381	AGTGTGTT	CAACGGGGCT	GGAGGATTTCCGTTGCT	CTCTGTGAGCCCTTTTATCTTTTCT	1440	
Db	2596	AGTGTGTT	CAACGGGGCT	GGAGGATTTCCGTTGCT	CTCTGTGAGCCCTTTTATCTTTTCT	2655	
QY	1441	CTGCTTGG	AGAGAAAGTCT	ATTCTTCA	TGAAAGGGATGCAGTTCAT	TAAGTGCAGCTGT	1500
Db	2656	CTGCTTGG	AGAGAAAGTCT	ATTCTTCA	TGAAAGGGATGCAGTTCAT	TAAGTGCAGCTGT	2715
QY	1501	AAAAATTC	CAAGG	TGTGCAT	TGGGTTTCTTTCACG	AGGCTTTTATTAATGGAAATATAG	1560
Db	2716	AAAAATTC	CAAGG	TGTGCAT	TGGGTTTCTTTCACG	AGGCTTTTATTAATGGAAATATAG	2775
QY	1561	GAAAGGAG	CTCATTTCT	TAGGCCGTTAAT	TTCACGGAGAAAGTGCATGAGCTTTTCTTT	1620	
Db	2776	GAAAGGAG	CTCATTTCT	TAGGCCGTTAAT	TTCACGGAGAAAGTGCATGAGCTTTTCTTT	2835	
QY	1621	CATGTCTT	CTGGGCAACT	ACTACG	CCCTGTGGTGGACCTTGCTTATG	CAACAAGGCTGAA	1680
Db	2836	CATGTCTT	CTGGGCAACT	ACTACG	CCCTGTGGTGGACCTTGCTTATG	CAACAAGGCTGAA	2895
QY	1681	AACCTTGA	ATCAGAGAG	CTCGGTTTCTTTCT	GGTTCTGCAT	TGGTTGGCTGTGGAC	1740
Db	2896	AACCTTGA	ATCAGAGAG	CTCGGTTTCTTTCT	GGTTCTGCAT	TGGTTGGCTGTGGAC	2955
QY	1741	CGTGGG	CAAGTGTCT	CTCTCCTTCC	TGGGACATAGTCTTCT	TGCTATTAAGACCTTTGCA	1800
Db	2956	CGTGGG	CAAGTGTCT	CTCTCCTTCC	TGGGACATAGTCTTCT	TGCTATTAAGACCTTTGCA	3015
QY	1801	GCTCTCG	GTGTTCTGTGA	CACTTCCCTGTGA	TTCTCTGTGAAGGGGGGAGTGTGAAGAGGG	1860	
Db	3016	GCTCTCG	GTGTTCTGTGA	CACTTCCCTGTGA	TTCTCTGTGAAGGGGGGAGTGTGAAGAGGG	3075	
QY	1861	AAGGAGG	CAAGCTGAG	AGCTGAGCCACAGGGGAGTGA	AGGGGGGACAGAAAGGACAG	1920	
Db	3076	AAGGAGG	CAAGCTGAG	AGCTGAGCCACAGGGGAGTGA	AGGGGGGACAGAAAGGACAG	3135	
QY	1921	CAGAGAG	CTGGGTGTCT	CACTCA	GTCTCACTGTATCACTTCACAGACCTGAGAGCC	1980	
Db	3136	CAGAGAG	CTGGGTGTCT	CACTCA	GTCTCACTGTATCACTTCACAGACCTGAGAGCC	3195	
QY	1981	CAATGCTT	CAGGAAGGCT	CAATGAAGCCACAGCC	CACTTTTCTTCCCTTCAAGATAGAC	2040	
Db	3196	CAATGCTT	CAGGAAGGCT	CAATGAAGCCACAGCC	CACTTTTCTTCCCTTCAAGATAGAC	3255	
QY	2041	AATGCA	TTTGGCAATTAAC	CAAAAAAGATG	CAGAGACTAATCTGTGTAGCTTTTGCTG	2100	
Db	3256	AATGCA	TTTGGCAATTAAC	CAAAAAAGATG	CAGAGACTAATCTGTGTAGCTTTTGCTG	3315	
QY	2101	GCAATTC	AAAAA	CTGGGCC	CAGACAGTGGAAATG	CCAGAGATTTGTTAACTTTTCAACC	2160
Db	3316	GCAATTC	AAAAA	CTGGGCC	CAGACAGTGGAAATG	CCAGAGATTTGTTAACTTTTCAACC	3375
QY	2161	TGACCG	AGC	CCCCACG	CACTCAGCAGTGA	CTGTGACAGCACGAGTGA	2220
Db	3376	TGACCG	AGC	CCCCACG	CACTCAGCAGTGA	CTGTGACAGCACGAGTGA	3435
QY	2221	AGGGAG	AGAGAA	AAAAAGAGG	AGATGTGTATATAG	CAAGAAAGAAAGACAGATTCATTTCAAG	2280
Db	3436	AGGGAG	AGAGAA	AAAAAGAGG	AGATGTGTATATAG	CAAGAAAGAAAGACAGATTCATTTCAAG	3495
QY	2281	GGCAGT	GGAAAT	TGACCA	CGGGAATTAATG	TATC	2340

Db	3496	GGCAATGGAAATTGACCAAGGAATTATAGTCCACGTGATCTGGGTTCTAGAGGACAGG	3555
Qy	2341	GCTAATATGTGGGGGAAAAAATCAGTTCAAGGAGTCCGGAGACCTGATTTTCTAATAC	2400
Db	3556	GCTAATATGTGGGGGAAAAAATCAGTTCAAGGAGAGTCCGGAGACCTGATTTTCTAATAC	3615
Qy	2401	TATATTTTCTTTTCAAGCTGAGTAATCTTGACCAAGTCAACAAGTATGTAATCTGAGCT	2460
Db	3616	TATATTTTCTTTTCAAGCTGAGTAATCTTGACCAAGTCAACAAGTATGTAATCTGAGCT	3675
Qy	2461	GTAAGATTACTAGTTTCTCCCTAATATGGAAGCTCTTTTCTCTGTGAGTTAGACAGCA	2520
Db	3676	GTAAGATTACTAGTTTCTCCCTAATATGGAAGCTCTTTTCTCTGTGAGTTAGACAGCA	3735
Qy	2521	AGGGCAATCCGGTTCCTTTTAAACAGAAAGAAAACATTCCTAAGATTAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCGGTTCCTTTTAAACAGAAAGAAAACATTCCTAAGATTAAGCCAAACAGAT	3795
Qy	2581	TCAAGCCTTAGGCTCTTGCTGACTATATGATGTGTTTTGAAAAATCATTTCAAGGATGT	2640
Db	3796	TCAAGCCTTAGGCTCTTGCTGACTATATGATGTGTTTTGAAAAATCATTTCAAGGATGT	3855
Qy	2641	TACTATCTGATTCCAGAAATGAGTACGATACCTTGCTGAGCTGTAACCAACACCAT	2700
Db	3856	TACTATCTGATTCCAGAAATGAGTACGATACCTTGCTGAGCTGTAACCAACACCAT	3915
Qy	2701	TTGTAAATGTCTCAAGTTCAGGCTTAACTGACAGAACCAATCAAAATGAATGAAATCTTT	2760
Db	3916	TTGTAAATGTCTCAAGTTCAGGCTTAACTGACAGAACCAATCAAAATGAATGAAATCTTT	3975
Qy	2761	AGAGCAAACTGTGTTTCTCACTCGAGAGTGAGTCTGCCAGGCGAGTTTGGAAATATTT	2820
Db	3976	AGAGCAAACTGTGTTTCTCACTCGAGAGTGAGTCTGCCAGGCGAGTTTGGAAATATTT	4035
Qy	2821	ACTTCACAAGATTGACACGTGTGTGTGATTAACAACATAAGTGTCCAAAGGCATC	2880
Db	4036	ACTTCACAAGATTGACACGTGTGTGTGATTAACAACATAAGTGTGTCCAAAGGCATC	4095
Qy	2881	ATTATTTTCAAGGCGCTTAAAGTTACTTGACAAGTTTGTATATTTATTTGGCTATTGCC	2940
Db	4096	ATTATTTTCAAGGCGCTTAAAGTTACTTGACAAGTTTGTATATTTATTTGGCTATTGCC	4155
Qy	2941	ATTTCCTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAGCAGGATTTATACCTAC	3000
Db	4156	ATTTCCTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAGCAGGATTTATTAACCTAC	4215
Qy	3001	AAGTCAGAAAGCCTGTGAATTTGAAATGAGAAAAATTAACATTTTGTTTTACACCTT	3066
Db	4216	AAGTCAGAAAGCCTGTGAATTTGAAATGAGAAAAATTAACATTTTGTTTTACACCTT	4275
Qy	3061	CTAATCAAAATTAACATTTTATTTTCATTGCGAAATGAGCCATTAACCAAAAGTGTAATA	3120
Db	4276	CTAATCAAAATTTAACAATTTTATTTTCATTGCGAAATGAGCCATTAACCAAAAGTGTAATA	4335
Qy	3181	GTTTGTTCAGATAAGTGTGAAGTGAATATTTATCTCAAAACATCTTTGAAATTTAGAC	3240
Db	4396	GTTTGTTCAGATAAGTGTGAAGTGAATATTTATCTCAAAACATCTTTGAAATTTAGAC	4455
Qy	3241	TCTGTGTGATCTGTGTTTTTAAACATTAATTAACAGTTTAAAAATTTGATATTTTGA	3300
Db	4456	TCTGTGTGATCTGTGTTTTTAAACATTAATTAACAGTTTAAAAATTTGATATTTTGA	4515
Qy	3301	TATCATATTTCAATTATCATTTGTTTCTTTGTAATCTATATTTTATATTTTGAACCA	3360
Db	4516	TATCATATTTCAATTATCATTTGTTTCTTTGTAATCTATATTTTATATTTTGAACCA	4575
Qy	3361	TCCTTTCTGAAAGGTTCCCAAGATTTTCAACAATAGGTTCTTGCAATGCACACACAG	3420

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Db      4576 TCTTCTGAGAGAGTTCCCAAGATTTCCCAATGAGTTCTTGGCATGCACACACAG 4635
Qy      3421 AGTAAAGACTGATTAGAGCTAACTTGACATTTGTGCTCGAGATGACAGACTGAATT 3480
Db      4636 AGTAAAGACTGATTAGAGCTAACTTGACATTTGTGCTCGAGATGACAGACTGAATT 4695
Qy      3481 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGAGGCTGAGGGGAAATCTGC 3540
Db      4696 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGAGGCTGAGGGGAAATCTGC 4755
Qy      3541 CGCTCTATAGGAAATGCTCTCCCTGAGACCTGAGAGGCTGCTGCTTGTGTTCTGAGCTG 3600
Db      4756 CGCTCTATAGGAAATGCTCTCCCTGAGACCTGAGAGGCTGCTGCTTGTGTTCTGAGCTG 4815
Qy      3601 GCTGTTATTTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
Db      4816 GCTGTTATTTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4875
Qy      3661 AGCATAGTGCCTGGCAGATGACAGTTCTCAATGAGTTTGCAGAGTGAATGGAATATTA 3720
Db      4876 AGCATAGTGCCTGGCAGATGACAGTTCTCAATGAGTTTGCAGAGTGAATGGAATATTA 4935
Qy      3721 ACTAGAAATATATCTCTGTTGAATTCAGCACACCAAGTCTGCTGCTGCTGCTGCTGCTG 3780
Db      4936 ACTAGAAATATATCTCTGTTGAATTCAGCACACCAAGTCTGCTGCTGCTGCTGCTGCTG 4995
Qy      3781 --GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3838
Db      4996 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5055
Qy      3839 GGGTATGAGTGATTAATTTGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTG 3898
Db      5056 GGGTATGAGTGATTAATTTGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTG 5115
Qy      3899 AAGTATTTTCTTAAGATTTTGTGTCGACGCTGAGAGGCAACCCCTCTGTCACAGCCCC 3958
Db      5116 AAGTATTTTCTTAAGATTTTGTGTCGACGCTGAGAGGCAACCCCTCTGTCACAGCCCC 5175
Qy      3959 ACCGAGCTCAGGTCGACCTCTGCTTCCCAATGAAAGGCTGCTCCCAATGAAATTA 4018
Db      5176 ACCGAGCTCAGGTCGACCTCTGCTTCCCAATGAAAGGCTGCTCCCAATGAAATTA 5235
Qy      4019 TAAACCTCTGAGCTCAGGATGAGCCAGCAAGGCAACCCATCCAGGCACTCTCAGC 4078
Db      5236 TAAACCTCTGAGCTCAGGATGAGCCAGCAAGGCAACCCATCCAGGCACTCTCAGC 5295
Qy      4079 ACAGC 4083
Db      5296 ACAGC 5300

RESULT 11
ID      AAV51363 standard; DNA; 5300 BP.
XX
AC      AAV51363;
XX
DT      27-OCT-1998 (first entry)
XX
DE      Human TIGR promoter mutant TIGRmt2 DNA.
XX
KM      TIGR; trabecular meshwork induced glucocorticoid response protein; human;
XX      diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
OS      Homo sapiens.
XX
XX      Synthetic.
XX
XX      Key
XX      mutation
XX      Location/Qualifiers
XX      /tag= a
XX      /note= "wild-type C is replaced with T"
XX
PN      WO9832850-A1.

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XX      30-JUL-1998.
PD      09-JAN-1998; 98MO-US000468.
XX
PF      28-JAN-1997; 97US-00791154.
XX
PR      26-SEP-1997; 97US-00938669.
XX
PA      (REGC ) UNIV CALIFORNIA.
XX
PI      Nguyen TD, Polansky JR, Chen P, Chen H;
XX      MPI; 1998-427946/36.
XX
PT      Use of TIGR nucleic acid sequences - used for, e.g. developing products
XX      for diagnosis, prognosis and treatment of glaucoma.
XX
PS      Disclosure; Fig 2; 105pp; English.
XX
CC      This sequence is a trabecular meshwork induced glucocorticoid response
CC      protein (TIGR) promoter mutant, TIGRmt2, which is used in a method for
CC      diagnosing glaucoma in a patient. The method involves the detection of
CC      polymorphisms whose presence is predictive of a mutation affecting TIGR
CC      response in the patient and can be diagnostic of glaucoma or steroid
CC      sensitivity. Base substitutions and base additions upstream of and within
CC      TIGR exons can also be used to diagnose glaucoma
XX
SQ      Sequence 5300 BP; 1482 A; 1151 C; 1235 G; 1432 T; 0 U; 0 Other;
XX
Query Match      67.8%; Score 4067.8; DB 2; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy      1 GCTCCACAGGAAGTCTCCCACTTGAAGCTTGCATCAGATGTTACAGCCAGAACTC 60
Db      1216 GCTCCACAGGAAGTCTCCCACTTGAAGCTTGCATCAGATGTTACAGCCAGAACTC 1275
Qy      61 CGTGAAGGATGAGGCTGCTGCTTACCTACCTGATGCTTACACCTGAGACTCACTGC 120
Db      1276 CGTGAAGGATGAGGCTGCTGCTTACCTACCTGATGCTTACACCTGAGACTCACTGC 1335
Qy      121 AACTCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCTCCCGGTAGCTGGAGCT 180
Db      1336 AACTCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCTCCCGGTAGCTGGAGCT 1395
Qy      181 AAGGCGCACGCGCGCTAATTTTGTATGTTAGTGAAGATGGGCTTACCATATTAG 240
Db      1396 AAGGCGCACGCGCGCTAATTTTGTATGTTAGTGAAGATGGGCTTACCATATTAG 1455
Qy      241 CCGGCTGCTCTTGAATCTCTGACCTCAGGATGATCCACCCACTAGCTCTCTAAAGTGC 300
Db      1456 CCGGCTGCTCTTGAATCTCTGACCTCAGGATGATCCACCCACTAGCTCTCTAAAGTGC 1515
Qy      301 TGGGATTAAGAGCATGATGACCGCGCCGCAAGGCTGATGTTTATAAGAAATAC 360
Db      1516 TGGGATTAAGAGCATGATGACCGCGCCGCAAGGCTGATGTTTATAAGAAATAC 1575
Qy      361 TTGAATGTTTATCTAACAACAGGAAACAGACAAAGCTGTGATTAATTTCAAGGATTC 420
Db      1576 TTGAATGTTTATCTAACAACAGGAAACAGACAAAGCTGTGATTAATTTCAAGGATTC 1635
Qy      421 TTGGATGAGGAAATGTCGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db      1636 TTGGATGAGGAAATGTCGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1695
Qy      481 CTTTCTTCCCTCATCTCATTTTCAAGCTAAGTATCAATTTTATTCACCATGCTTTTGG 540
Db      1696 CTTTCTTCCCTCATCTCATTTTCAAGCTAAGTATCAATTTTATTCACCATGCTTTTGG 1755
Qy      541 GTAAGCTTCACATGTTTACTGAATAAGATATCAATTAACATGTTCAATTTGGGGCCA 600
Db      1756 GTAAGCTTCACATGTTTACTGAATAAGATATCAATTAACATGTTCAATTTGGGGCCA 1815

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QY 601 TCTGTGTGTGTATAGGGAGAGAGGATACCCAGAGACTCTTTGAAGCCCCGGCAG 660
 Db 1816 TCTGTGTGTGTATAGGGAGAGAGGACATCCAGAGACTCTTTGAAGCCCCGGCAG 1875
 QY 661 AGGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTGTCTGAGCA 720
 Db 1876 AGGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTGTCTGAGCA 1935
 QY 721 ACCTGCAAGCCCGTGCACCTGGTGTGTTTGTATACACTCTCTAAGGACCTGTGTCTTCT 780
 Db 1936 ACCTGCAAGCCCGTGCACCTGGTGTGTTTGTATACACTCTCTAAGGACCTGTGTCTTCT 1995
 QY 781 ATTCTGTGTGTACTGTTCAATTCATCCAGGCAATTCATGACAAATTTATTAAGTACTTATA 840
 Db 1996 ATTCTGTGTGTACTGTTCAATTCATCCAGGCAATTCATGACAAATTTATTAAGTACTTATA 2055
 QY 841 TTGTGCAAGACACAGAGACAAAATGTGTAGGCAAGACGTCATGGCCCTTAACCTTGTGAG 900
 Db 2056 TTGTGCAAGACACAGAGACAAAATGTGTAGGCAAGACGTCATGGCCCTTAACCTTGTGAG 2115
 QY 901 GTGACAGTTTCTCATGGAAGAGTGTGAGAAAGAAATTAATAGCCAGCCAACTTAAACCA 960
 Db 2116 GTGACAGTTTCTCATGGAAGAGTGTGAGAAAGAAATTAATAGCCAGCCAACTTAAACCA 2175
 QY 961 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGAGCATCCCTTAACAA 1020
 Db 2176 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGAGCATCCCTTAACAA 2235
 QY 1021 GGGCACCTCTCTAGAGCCCTCTGTCTCTCATTCGTGCCCCGAGAGCCCCAGCCCGAGT 1080
 Db 2236 GGGCACCTCTCTAGAGCCCTCTGTCTCTCATTCGTGCCCCGAGAGCCCCAGCCCGAGT 2295
 QY 1081 CTTCCAAAGCCTCTCTCCATCATGATCAAGAGCTGAGAGCTGAGCTCGCTTCCGCTG 1140
 Db 2296 CTTCCAAAGCCTCTCTCCATCATGATCAAGAGCTGAGAGCTGAGCTCGCTTCCGCTG 2355
 QY 1141 AATCGTCTGTGTGATCTGAGCTGAGAGCTCTTGTGCTTCAGAGCTTCAGAAAGAAATG 1200
 Db 2356 AATCGTCTGTGTGATCTGAGCTGAGAGCTCTTGTGCTTCAGAGCTTCAGAAAGAAATG 2415
 QY 1201 AAGAGGAAACTAGTCTTAACGAGAAATCTGAGAGGGGACATGTGTTTCTCAGAGGAAAGG 1260
 Db 2416 AAGAGGAAACTAGTCTTAACGAGAAATCTGAGAGGGGACATGTGTTTCTCAGAGGAAAGG 2475
 QY 1261 GCTCCACGTCAGAGGAAATTCAGAGGGTGGGAACTGACAGGAGAGTGGGAAAGCTGGAGC 1320
 Db 2476 GCTCCACGTCAGAGGAAATTCAGAGGGTGGGAACTGACAGGAGAGTGGGAAAGCTGGAGC 2535
 QY 1321 TGAAGCGGTGTGAAAGGACAGAGAGGTGAAAGGGGCAAGCTGAGAGCTCCAGATGTTT 1380
 Db 2536 TGAAGCGGTGTGAAAGGACAGAGAGGTGAAAGGGGCAAGCTGAGAGCTCCAGATGTTT 2595
 QY 1381 AGTGTGTGTCAAGGGGCTGGAGATTTTCCGTGTCTCTGTGAGCTTTTATCTTTTCT 1440
 Db 2596 AGTGTGTGTCAAGGGGCTGGAGATTTTCCGTGTCTCTGTGAGCTTTTATCTTTTCT 2655
 QY 1441 CTGCTTGAAGAGAAAGATCTATTCTATGAAGAGATGCAATTTCTATAAGTCAAGCTGT 1500
 Db 2656 CTGCTTGAAGAGAAAGATCTATTCTATGAAGAGATGCAATTTCTATAAGTCAAGCTGT 2715
 QY 1501 AAAATTCAGAGGTGTGCATGGTGTTCCTTCAGAAAGGCTTTTATTTAATGGAAATATAG 1560
 Db 2716 AAAATTCAGAGGTGTGCATGGTGTTCCTTCAGAAAGGCTTTTATTTAATGGAAATATAG 2775
 QY 1561 GAAAGCAGCTCATTTTCTTAGGCGGTAAATTCAGAGAAAGTGAAGTGGAGTCTTTTCTT 1620
 Db 2776 GAAAGCAGCTCATTTTCTTAGGCGGTAAATTCAGAGAAAGTGAAGTGGAGTCTTTTCTT 2835
 QY 1621 CATGTCTTCTGGCACTACTAGCCCTGTGTGAGCTTGCTTATGCAAGAGCGTGCAG 1680
 Db 2836 CATGTCTTCTGGCACTACTAGCCCTGTGTGAGCTTGCTTATGCAAGAGCGTGCAG 2895
 QY 1681 AACCTTGAATCAGAGACTCGGTTTCTTCTGTGTTCTGCCAATGGTGTGCTGTGCAG 1740

Db 2896 AACCTTGAATCAGAGACTCGGTTTCTTCTGTGTTCTGCATGTGTGCTGTGCAG 2955
 QY 1741 CGTGGGCAAGTGTCTCTTCCCTGGGCCATAGTCTTCTCTGTATTAAGACCTTGCA 1800
 Db 2956 CGTGGGCAAGTGTCTCTTCCCTGGGCCATAGTCTTCTCTGTATTAAGACCTTGCA 3015
 QY 1801 GCTCTGTGTGTGTGAAACATTCCTGTGTATTTCTGTGTAGGGGGAGTGTGAGAGGG 1860
 Db 3016 GCTCTGTGTGTGTGAAACATTCCTGTGTATTTCTGTGTAGGGGGAGTGTGAGAGGG 3075
 QY 1861 AAGAGGCAAGCTGTGAGACGCTGAGCCACAGGGGAAGTGTGAGGGGGACAGAAAGCCAG 1920
 Db 3076 AAGAGGCAAGCTGTGAGACGCTGAGCCACAGGGGAAGTGTGAGGGGGACAGAAAGCCAG 3135
 QY 1921 CAGAAGCTGGGTGCTCATGCTAGCTCTCACTGATCAGCTCAGAGCTCCAGAACGAGCCA 1980
 Db 3136 CAGAAGCTGGGTGCTCATGCTAGCTCTCACTGATCAGCTCAGAGCTCCAGAACGAGCCA 3195
 QY 1981 CAATGCTTCAGAAAGCTCAATGAACCCACAGCCACATTTTCTTCCCTTAAGCATAGAC 2040
 Db 3196 CAATGCTTCAGAAAGCTCAATGAACCCACAGCCACATTTTCTTCCCTTAAGCATAGAC 3255
 QY 2041 AATGCAATTTGCCAATTAACCAAAAGAAATGCAAGACTAATCTGTGTGTAGCTTTGTCTG 2100
 Db 3256 AATGCAATTTGCCAATTAACCAAAAGAAATGCAAGACTAATCTGTGTGTAGCTTTGTCTG 3315
 QY 2101 GCATTCAAAACTGTGGGCGAGAGCAAGTGAAGAAATGCGAGAAATGTTTAACTTTTCAACC 2160
 Db 3316 GCATTCAAAACTGTGGGCGAGAGCAAGTGAAGAAATGCGAGAAATGTTTAACTTTTCAACC 3375
 QY 2161 TGACCAAGCACCCCAAGCAGCTCAGCAGTACTGTGTGACAGAGCGAGTACCTCAGAGCG 2220
 Db 3376 TGACCAAGCACCCCAAGCAGCTCAGCAGTACTGTGTGACAGAGCGAGTACCTCAGAGCG 3435
 QY 2221 AGGGAGGAGAAAGAAAGAGAGGATAGTATAGAGCAAGAAAGACAGATTCTTCAAG 2280
 Db 3436 AGGGAGGAGAAAGAAAGAGAGGATAGTATAGAGCAAGAAAGACAGATTCTTCAAG 3495
 QY 2281 GGCAGTGGGAATTTGACCAAGAGATTAATAGTCCAGGTATCTGTGGTCTTGAAGAGCCAG 2340
 Db 3496 GGCAGTGGGAATTTGACCAAGAGATTAATAGTCCAGGTATCTGTGGTCTTGAAGAGCCAG 3555
 QY 2341 GCTATATTGTGGGGGAAATTAATCAATCAAGGAGAGTGGGAGACCTGATTTCTAATAC 2400
 Db 3556 GCTATATTGTGGGGGAAATTAATCAATCAAGGAGAGTGGGAGACCTGATTTCTAATAC 3615
 QY 2401 TATATTTTCTTTACAGCTGAGTATTTCTGAGCAATCAAGTATGTAATGAGGCT 2460
 Db 3616 TATATTTTCTTTACAGCTGAGTATTTCTGAGCAATCAAGTATGTAATGAGGCT 3675
 QY 2461 GTAAGTACTAGTATTTTCTCCTAATTAAGAACTTTTCTCTGTGAGTATGAGCAGCA 2520
 Db 3676 GTAAGTACTAGTATTTTCTCCTAATTAAGAACTTTTCTCTGTGAGTATGAGCAGCA 3735
 QY 2521 AGGGCAATCCGTTTCTTTTAAACAGAGAAACAATTCCTAAGAGTAAAGCCAAACAGAT 2580
 Db 3736 AGGGCAATCCGTTTCTTTTAAACAGAGAAACAATTCCTAAGAGTAAAGCCAAACAGAT 3795
 QY 2581 TCAAGCTTAGTCTTGTGAGCTATATGATGGTGTGTTTGAAGAAATCATTTCAAGCAATTT 2640
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 Db 3856 TACTATCTGATTCAAGAAATGAGTACTAGTACCTTTGTGCTGAGCTTAAACAAACCCAT 3915
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 QY 2761 AAGCAAACTGTGTGTTCTCAGCTGTGAGGTGAGTCTGCAAGGGAGTTTGAATATTTT 2820

D	3976	AGAGCAAACTGCTTTCTCCACTCTCGAGGTGAGTCTCCAGGGCAGTTTGAAATATTT	4035
Q	2821	ACTTCAACAATATGACACTGTGTGTGATTAACAATAAGTGTCCAAAGCAATC	2880
D	4036	ACTTCAACAATATGACACTGTGTGTGATTAACAATAAGTGTCCAAAGCAATC	4095
Q	2881	ATTATTTCAAGGCGCTTAAGTACTTCTGACAGTTTGGTATATTTATTTGGCTATGGC	2940
D	4096	ATTATTTCAAGGCGCTTAAGTACTTCTGACAGTTTGGTATATTTATTTGGCTATGGC	4155
Q	2941	ATTGCTTTTGTTTTTCTCTTGGGTTATTAATGTAAAGCAGGATTAATTAACCTAC	3000
D	4156	ATTGCTTTTGTTTTTCTCTTGGGTTATTAATGTAAAGCAGGATTAATTAACCTAC	4215
Q	3001	AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTACATTTTGTATTTTACCACTT	3060
D	4216	AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTACATTTTGTATTTTACCACTT	4275
Q	3061	CTAATCTAATTTAATCAATTTTATTTCCATTGGCAATGAGCCATTAACCTCAAAAGGTATA	3120
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Q	3121	ACAGTACCTGTGATTTTGTCAATTAACAATAGAAATCAACAAGCATTTTATCTATTTACA	3180
D	4336	ACAGTACCTGTGATTTTGTCAATTAACAATAGAAATCAACAAGCATTTTATCTATTTACA	4395
Q	3181	GTGTGTGCAGATACGTTGTGAATGAATATTTATCTCAAAACTACTTTGAAATTTAGAC	3240
D	4396	GTGTGTGCAGATACGTTGTGAATGAATATTTATCTCAAAACTACTTTGAAATTTAGAC	4455
Q	3241	TCCGCTCGATCTTGTTTTTTAAATATTTAATTAACATGTTTAAATTTGATATTTTGA	3300
D	4456	TCCGCTCGATCTTGTTTTTTAAATATTTAATTAACATGTTTAAATTTGATATTTTGA	4515
Q	3301	TAATCATATTTCAATTAATTTGTTTCTTTGGTATCTAATATTTATTAATTTGAAATA	3360
D	4516	TAATCATATTTCAATTAATTTGTTTCTTTGGTATCTAATATTTATTAATTTGAAATA	4575
Q	3361	TCTTCTGAGAAAGTTCCCGAGATTTCAACCAATGAGGTTCTTGGCATGCACACACAG	3420
D	4576	TCTTCTGAGAAAGTTCCCGAGATTTCAACCAATGAGGTTCTTGGCATGCACACACAG	4635
Q	3421	AGTAAAGATCTGATTTAGAGGCTTAACATTGACATTTGGTGCCTGAGATGCAGACTGAATT	3480
D	4636	AGTAAAGATCTGATTTAGAGGCTTAACATTGACATTTGGTGCCTGAGATGCAGACTGAATT	4695
Q	3481	AGAAAGTCTCCCAAGATTAACAGCTTTTAAAGCTAAGGGGTGAAGGGGGGAAATCTGC	3540
D	4696	AGAAAGTCTCCCAAGATTAACAGCTTTTAAAGCTAAGGGGTGAAGGGGGGAAATCTGC	4755
Q	3541	CGCTTCTAATAGAAATGCTCCCTCGAGAGCTGTAGGGTGTCTCTTGTATTTCTGCTG	3600
D	4756	CGCTTCTAATAGAAATGCTCCCTCGAGAGCTGTAGGGTGTCTCTTGTATTTCTGCTG	4815
Q	3601	GCTGTATATTTTCTCTGTCCCTGCTAGCTTTAAAGACCTTGTGATCTCCAGTTCT	3660
D	4816	GCTGTATATTTTCTCTGTCCCTGCTAGCTTTAAAGACCTTGTGATCTCCAGTTCT	4875
Q	3661	AGCATATGAGCTCGGACACATGCAAGTTCATAGATTTGACAGATGAATGAAATATTA	3720
D	4876	AGCATATGAGCTCGGACACATGCAAGTTCATAGATTTGACAGATGAATGAAATATTA	4935
Q	3721	ACTAGAAATATATCTTGTGTAAATACAGACACAGATAGTCTGAGTAAAGTGTGTAC	3780
D	4936	ACTAGAAATATATCTTGTGTAAATACAGACACAGATAGTCTGAGTAAAGTGTGTAC	4995
Q	3781	--GTGTGTGTGTGTGTGTGTGTGTGTAAACAAGGTGAGATATAGAACTATTTATG	3838
D	4996	GTGTGTGTGTGTGTGTGTGTGTGTGTAAACAAGGTGAGATATAGAACTATTTATG	5055
Q	3839	GGGATATGGGTCATTAATTTGGAGATGTTCTTTTAAAGAAATCTCCAAACAGACTTCTGG	3898
D	5056	GGGATATGGGTCATTAATTTGGAGATGTTCTTTTAAAGAAATCTCCAAACAGACTTCTGG	5115

[illegible]

RESULT 12
AAV51366
ID AAV51366 standard; DNA; 5300 BP.
vv

DT 27-OCT-1998 (first entry)

Human TIGR promoter mutant TIGRmt5 DNA.

TIGR; trabecular meshwork induced glucocorticoid response protein; human; diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.

Homo sapiens.
Synthetic.

Key	Location/Qualifiers
mutation	4262

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/note= "Wild-type G is replaced with A"
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W09832850-A1.

30-JUL-1998.

09-JAN-1998; 98WO-US000468.

28-JAN-1997; 97US-00791154.

(REGC) UNIV CALIFORNIA.

Nguyen TD, Polansky JR, Chen P, Chen H;

WPI; 1998-427946/36.

Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma.

Disclosure; Fig 2; 105pp; English.

CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) promoter mutant, TIGRmt5, which is used in a method for
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CC response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
CC TIGR exons can also be used to diagnose glaucoma

Sequence 5300 BP; 1483 A; 1152 C; 1234 G; 1431 T; 0 U; 0 Other;

Query Match	67.8%;	Score 4067.8;	DB 2;	Length 5300;
Best Local Similarly	99.9%;	Pred. No. 0;		
Matches 4081; Conservative	0;	Mismatches 2;	Indels 2;	Gaps 1;

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 QY 121 AACCTGTGCTCCAGAGTTCAAGCAATTCTCCGTCTGAGCTCCCGAGTACTGAGACT 180
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 QY 241 CCGGCTGTCTTTGAATCTCTGACCTCAAGGTATCCACCACTCAAGCTCCTTAAAGTGC 300
 Db 1456 CCGGCTGTCTTTGAATCTCTGACCTCAAGGTATCCACCACTCAAGCTCCTTAAAGTGC 1515
 QY 301 TGGGATTAAGGATGATGACACCGGCGCCGAGGAGGTCACTGTTTAAATAGAAATAC 360
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 QY 601 TCTGTGTGTGTATATAGGGAAGAGGACATACCCAGAGACTCTTTGAAGCCCCCGGCGAG 660
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 QY 781 AATTCTGTGTACTCGTTCAATTCACAGGCAATTCATTAACAATTTATGATGATCTTAA 840
 Db 1996 AATTCTGTGTACTCGTTCAATTCACAGGCAATTCATTAACAATTTATGATGATCTTAA 2055
 QY 841 TCTGCAGACACAGAGCAAAATGATGAGCAAAAGCATGAGCCCTTACCTTGGTGGAG 900
 Db 2056 TCTGCAGACACAGAGCAAAATGATGAGCAAAAGCATGAGCCCTTACCTTGGTGGAG 2115
 QY 901 GTGACAGTTTCTCATGGAAGAAGTGCAGAAAGAAATTAATAGCCAGCCAACTTAAACCA 960
 Db 2116 GTGACAGTTTCTCATGGAAGAAGTGCAGAAAGAAATTAATAGCCAGCCAACTTAAACCA 2175
 QY 961 GTGCTGAAAAGAAATTAACAACATTTTGAAGATTGTGGCAGCATCCCTTAAACA 1020
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 Db 2416 AGAGGGAACCTAGTCTAACGGAATCTGAGGAGGACAGTGTTCCTCAGAGGAAAGG 2475
 QY 1261 GCTTCACGTCAGAGAAATTCAGAGAGTGGGACCTGCAAGAGTGGGACCGCTGGGAC 1320
 Db 2476 GCTTCACGTCAGAGAAATTCAGAGAGTGGGACCTGCAAGAGTGGGACCGCTGGGAC 2535
 QY 1321 TGAAGGAGTGTGTAAGGACAGAAAGTGAAGAAAGGCAAGCTGAAGCTGCCAGATGTC 1380
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 Db 2596 AGTGTGTTCAAGGAGGCTGAGAGTGTTCCTGTGCTTCCGTGAGCTTTTATCTTTTCT 2655
 QY 1441 CTGCTTGAAGAGAAAGTCTATTTCATGAAGGATGCAATTCATTAAGTCAAGCTT 1500
 Db 2656 CTGCTTGAAGAGAAAGTCTATTTCATGAAGGATGCAATTCATTAAGTCAAGCTT 2715
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 Db 2716 AAAATTCAGAGGTGACATGGGTTTCTTCCAGAGGCTTTATTTAAATGGGAATATAG 2775
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 Db 3076 AAGGAGGAGAGCTGAGACAGTGAAGCAAGGGAGGTGAGGGGGAACAGAAAGGCAAG 3135
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 Db 3136 CAGAACTGGGTGCTCATCAAGTCTCATGATCACTGACACTCCAGAGCCGAGAGCA 3195
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 QY 2101 GCATTCAAAATCTGGGCGAGAGCAAGTGAAGAAATGCGAGAAATGTTAACTTTTCAACC 2160
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XX Key Location/Qualifiers
 FT mutation 4337
 FT /*tag= a
 FT /note= "Wild type C is replaced by G"
 PN MO9832850-A1.
 PD 30-JUL-1998.
 XX
 XX 09-JAN-1998; 98W-US000468.
 XX
 XX 28-JAN-1997; 97US-00791154.
 PR 26-SEP-1997; 97US-00938669.
 XX
 PA (RBSC) UNIV CALIFORNIA.
 XX
 PI Nguyen TD, Polansky JR, Chen P, Chen H;
 XX
 XX WPI, 1998-427946/36.
 DR
 XX Use of TIGR nucleic acid sequences - used for, e.g. developing products
 PT for diagnosis, prognosis and treatment of glaucoma.
 XX
 PS Disclosure; Fig 2; 105p; English.
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 CC response in the patient and can be diagnostic of glaucoma or steroid
 CC sensitivity. Base substitutions and base additions upstream of and within
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 CC
 XX
 XX Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 U; 0 Other;
 SQ
 Query Match 67.8%; Score 4067.8; DB 2; Length 5300;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

DB 1696 CTTTCTCCCTCATCCCTCATTTTCAGGCTAAGTTACCATTTTATTCACCATGCTTTTGTG 1755
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 QY 601 TCTGTGTGTGTGTATAGGAGAGAGGAGCATACCCAGAGACTCCTTGAAGCCCCGGCAG 660
 DB 1816 TCTGTGTGTGTGTATAGGAGAGAGGAGCATACCCAGAGACTCCTTGAAGCCCCGGCAG 1875
 QY 661 AGTTTCTCTCCAGCTGGGGAGCCCTCGAAGCACCAGGGGTCTGGGTCTCTGAGCA 720
 DB 1876 AGTTTCTCTCCAGCTGGGGAGCCCTCGAAGCACCAGGGGTCTGGGTCTCTGAGCA 1935
 QY 721 ACCTCGACGCCCCGCGACATGCTGTTTGTATACCTCTAGGAGCTGTGCTTCT 780
 DB 1936 ACCTCGACGCCCCGCGACATGCTGTTTGTATACCTCTAGGAGCTGTGCTTCT 1995
 QY 781 ATTTCTGTGTGACTCGTTTCATTTCATCCAGGCAATTCATGACATTTATAGTACTATA 840
 DB 1996 ATTTCTGTGTGACTCGTTTCATTTCATCCAGGCAATTCATGACATTTATAGTACTATA 2055
 QY 841 TCTGCCAGACACCAAGACAAATGTGAGCAAAAGCTCATCTGCCCTTACTTGTGAG 900
 DB 2056 TCTGCCAGACACCAAGACAAATGTGAGCAAAAGCTCATCTGCCCTTACTTGTGAG 2115
 QY 901 GTGACAGTTTCTCATNGAAGACGTGCAAGAAATTAATAGCAGCCCACTTAACCCA 960
 DB 2116 GTGACAGTTTCTCATNGAAGACGTGCAAGAAATTAATAGCAGCCCACTTAACCCA 2175
 QY 961 GTGCTGAAGAAAGAAATATAACACACTCTTGAAGATTTGTGCGCAGCATCCTTAACA 1020
 DB 2176 GTGCTGAAGAAAGAAATATAACACACTCTTGAAGATTTGTGCGCAGCATCCTTAACA 2235
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 DB 2236 GGCACCTCCCTAAGGCCCCCTGCTGCTCATGTGTCGCGAGGCCCAAGCCCAAGT 2295
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 DB 2296 CTTCCAAACCTTCCTTCATCAATGACAGAGGCTGAGCTGGCTGCTCCGCTG 2355
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 DB 2356 AATGCTCTGTGTGATCTGAGCTGGAAGACTCCTTGACTCCAGGCTCCAGAAAGAAATG 2415
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 DB 2416 AGAGGAAACTAGTTAACGAGAAATCTGAGGGGACAGTGTTCCTCAGAGGAAAGG 2475
 QY 1261 GCTTCAAGCTCAGAGAAATTCAGAGAGTGGGAGCTGCAAGGAGTGGGAGCGCTGGGG 1320
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 QY 1381 AGTGTGTTCACGAGGCTGGAGAGTTTCCGTTGCTTCTGTGAGCTTTTATCTTTTCT 1440
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Qy 1741 CGTGGGCAAGTCTCTCCCTCCCTGGGCAATAGTCTTCTCTGTATTAAGACCTTTGCA 1800
Db 2956 CGTGGGCAAGTCTCTCCCTCCCTGGGCAATAGTCTTCTCTGTATTAAGACCTTTGCA 3015
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Db 3016 GCTCTGCTGTCTGTGAACACTTCCCTGTGATTTCTGTGAGGGGGGAGTTTGAGAGGG 3075
Qy 1861 AAGAGGCAAGCTGAGAGCTGAGCCACAGGGGAGGTGAGGGGACAGAAAGGACG 1920
Db 3076 AAGAGGCAAGCTGAGAGCTGAGCCACAGGGGAGGTGAGGGGACAGAAAGGACG 3135
Qy 1921 CAGAACCTGGGTCTCATAGTCTCACTGATCACTGACTCCAGACCGAGGCCA 1980
Db 3136 CAGAACCTGGGTCTCATAGTCTCACTGATCACTGACTCCAGAGCCAGAGGCCA 3195
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Db 3196 CAATGCTTCAAGAAAGCTCAATGACCCAAACAGCCCACTTTTCCCTTAAGCATAGAC 3255
Qy 2041 AATGCAATTTGCCAATTAACCAAAAGATGACAGACTGAGTGTAGCTTTTGCCTG 2100
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Qy 2761 AGAGCAAACTGTGTCTCCACTCTGAGAGTGTGCTGACAGGCGAGTTGGAATATTT 2820
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2006, 01:29:42 ; Search time 20443 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: gb_est7:*
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11: gb_gse83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	628.2	10.5	937	3	B1818249 603032468
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6	607	10.1	607	7	CV574677 ce27d04.y
7	604	10.1	1515	10	AY16721
8	598.4	10.0	608	3	BP382502
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ALIGNMENTS

RESULT 1
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LOCUS 603038284F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179076 5',
DEFINITION mRNA sequence.

ACCESSION B1821411
VERSION B1821411.1 GI:15932961
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 756)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11446 row: h column: 21
High quality sequence stop: 754.

FEATURES

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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (BcoRI site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gubser (Invitrogen). Research Genetics tracking code

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RESULT 3
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LOCUS CD172504
DEFINITION AGENCOURT 14064069 NIH_MGC 181 Homo sapiens cDNA clone
IMAGE:30375751 5', mRNA sequence.
CD172504
CD172504.1 GI:30854135

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 877)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloned distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM437 row: e column: 08
High quality sequence stop: 739.
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/note="Vector: PCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 Kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC library."

ORIGIN
Query Match 10.9%; Score 653.8; DB 6; Length 877;
Best Local Similarity 99.7%; Pred.No.3.2e-104;
Matches 655; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 4069 ACCTCTACAGCAGAGAGCTTCCAGAGAGCTCCACCAAGCTTGCATGAGGTTTC 4128
QY 1 ACCTCTACAGCAGAGAGCTTCCAGAGAGAGCTCCACCAAGCTTGCATGAGGTTTC 60
Db 4129 TTCTGTGACGTTGCTGACGCTTTGGGCGTGAATGCCAGCTGTCCAGCTGCTTCTG 4188
QY 61 TTCTGTGACGTTGCTGACGCTTTGGGCGTGAATGCCAGCTGTCCAGCTGCTGCTTCTG 120

QY 4189 GCTTGCCTGTGTGGATGTGTGGGGCCAGACAGCTCAGTCCAGGAAGCCAAATGACCG 4248
Db 121 GCTTGCCTGTGTGTGGATGTGTGGGGCCAGACAGCTCAGTCCAGGAAGCCAAATGACCG 180
QY 4249 AGTGCCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAATCAGCTGCCAGAG 4308
Db 181 AGTGCCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAATCAGCTGCCAGAG 240
QY 4309 CAGAGCCAGGCCAATGTCAATCATCATTAATTACAGAGAGACAGAGACCCAAAGCTTA 4368
Db 241 CAGAGCCAGGCCAATGTCAATCATCATTAATTACAGAGAGACAGAGACCCAAAGCTTA 300
QY 4369 GACCTGAGGCGCACCAAAAGCTGCACTCAGTCCCTGAGAGAGCTTCCACCAATTGACC 4428
Db 301 GACCTGAGGCGCACCAAAAGCTGCACTCAGTCCCTGAGAGAGCTTCCACCAATTGACC 360
QY 4429 TTGACACAGGCTGCCAGGCGCCAGAGAGCCAGAGAGGGGCTGCAGAGGAGCTGGGACCC 4488
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QY 4489 CTGAGGCGGAGGCGGAGACCACTGGAACCCAAACAGAGAGTTGAGACTGCTTACGAC 4548
Db 421 CTGAGGCGGAGGCGGAGACCACTGGAACCCAAACAGAGAGTTGAGACTGCTTACGAC 480
QY 4549 AACCTCCTCCGAGCAAGTCACTTCTGAGAGAGAGAGAGGCACTAAGGCAAGAAAT 4608
Db 481 AACCTCCTCCGAGCAAGTCACTTCTGAGAGAGAGAGAGGCACTAAGGCAAGAAAT 540
QY 4609 GAGATCTGGCCAGAGAGTTGGAAGACGACGACGAGAGGTAGCAGAGCTGAGAGGGGC 4668
Db 541 GAGATCTGGCCAGAGAGTTGGAAGACGACGACGAGAGGTAGCAGAGCTGAGAGGGGC 600
QY 4669 CAGTGTCCCGACAGCCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGAGAAAGT 4725
Db 601 CAGTGTCCCGACAGCCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGAGAAAGT 657

RESULT 4
B1818249 937 bp mRNA linear EST 04-OCT-2001
LOCUS B1818249
DEFINITION 603032468P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173673 5',
mRNA sequence.
B1818249
B1818249.1 GI:15928689

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 937)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloned distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1432 row: g column: 18
High quality sequence stop: 839.
Location/Qualifiers
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FEATURES
source

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OY		4471	CAGAAGGAGCTGGGCGCACCCCTTGAGGCGGAGCGGGAACAAGTCGAAATCCCAAACCAAGAG	4530
Db		361	CAGAGGGAGCTGGGCGCACCCCTTGAGGCGGAGCGGGAACAAGTCGAAATCCCAAACCAAGAG	420
OY		4511	TTGGAGACTGCTCTACAGCAACTCTCTCCGAGACAAAGTCAGTTCTTGGAGAAAGAGAAAG	4590
Db		421	TTGGAGACTGCTCTACAGCAACTCTCTCCGAGACAAAGTCAGTTCTTGGAGAAAGAGAAAG	480
OY		4591	CGACTTAAGCAAGAAAATAGAAATCTGGCCAGAGAGTTTGAAAGAGAGACGACAGAGAGTA	4656
Db		481	CGACTTAAGCAAGAAAATAGAAATCTGGCCAGAGAGTTTGAAAGAGAGACGACAGAGAGTA	540
OY		4651	GCAAGGCTGAGAAGGGGGCCAGTGTCTCCGAGACCCGAGACACTGTCTGGGGCTGTGCACCA	4710
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OY		4711	GGCTTCAGAGAAAGT 4725	
Db		601	GGCTTCAGAGAAAGT 615	
RESULT 6				
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DEFINITION		oe27d04.y1 Human keratococcus cornea, unamplified, (od/oe) Homo sapiens cDNA clone oe27d04 5', mRNA sequence.		
ACCESSION		CVS74677		
VERSION		CVS74677.1 GI:54479490		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1 (bases 1 to 607)		
AUTHORS		Rabinowitz,Y., Dong,L. and Wislow,G.		
TITLE		Expressed sequence tag analysis of human keratococcus cornea unpublished (2004)		
JOURNAL		Contact: Wislow G		
COMMENT		Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: grame@helix.nih.gov Plate: 27 row: d column: 04 Seg primer: M13RPI reverse primer (ABI). Location/Qualifiers		
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		/clone="oe27d04"		
		/tissue_type="Cornea"		
		/dev_stage="Adult"		
		/lab_host="EMDH10B"		
		/clone_idb="Human keratococcus cornea, unamplified, (od/oe)"		
		/note="Organ: Eye; Vector: pCMVSPORT6; Approximately 40ug total RNA was extracted from 7 adult human keratococcus corneas. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTATTCTAGATCCGAGCGGCGCCCT(7)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on		

the unamplified library at the NIH Intramural Sequencing Center (NISC). "

Query Match	Similarity	10.1%	Score 607	DB 7	Length 607
Best Local	Similarity	100.0%	Pred. No. 5,4e-96		
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				Indels	0
				Gaps	0
Qy	4073	CTCAGCAGCAGAGCTTTCCAGAGAAAGCTCCACAAAGCCTCTGCAATGAGGTTCTT			4133
Db	1	CTCAGCAGCAGAGAGCTTTCCAGAGAAAGCTCCACAAAGCCTCTGCAATGAGGTTCTT			60
Qy	4133	GTGACGTTGTGTGACGTTTGGGCTTGAGATGCGACGTTCTGACTGTGCTTCTTGCGCT			4199
Db	61	GTGACGTTGTGTGACGTTTGGGCTTGAGATGCGACGTTCTGACTGTGCTTCTTGCGCT			120
Qy	4193	GCCGTGTGTGGGATGTGGGGCCCGAGACAGCTCAGCTCAGGAAAGCCAAATGACAGATG			4255
Db	121	GCCGTGTGTGGGATGTGGGGCCCGAGACAGCTCAGCTCAGGAAAGCCAAATGACAGATG			180
Qy	4253	GCCGATCCAGATATACCTTCAGTGTGCGCAGTCCCAATGAATCCAGTCCCGACAGAGA			4312
Db	181	GCCGATCCAGATATACCTTCAGTGTGCGCAGTCCCAATGAATCCAGTCCCGACAGAGA			240
Qy	4313	GCCAGGCGATGTGATCATCATTAACCTTACAGAGACAGAGACCCCAAGCTTGAAC			4372
Db	241	GCCAGGCGATGTGATCATCATTAACCTTACAGAGACAGAGACCCCAAGCTTGAAC			300
Qy	4373	TGAGAGCCACAAAGCTCAGCTCAGCTCCCTGAGAGACCTTCCACCAATTTGACCTTGG			4433
Db	301	TGAGAGCCACAAAGCTCAGCTCAGCTCCCTGAGAGACCTTCCACCAATTTGACCTTGG			360
Qy	4433	ACCAAGGCTGCCAGGCCCCCAGAGAGCCCAAGAGGGGGCTGCGAGAGGAGTGGGCACTGA			4493
Db	361	ACCAAGGCTGCCAGGCCCCCAGAGAGCCCAAGAGGGGGCTGCGAGAGGAGTGGGCACTGA			420
Qy	4493	GGCGGAGCGGAGACAGCTGGAACCCCAACCAAGAGTTGGAGACTGCCATACAGCAAC			4555
Db	421	GGCGGAGCGGAGACAGCTGGAACCCCAACCAAGAGTTGGAGACTGCCATACAGCAAC			480
Qy	4553	TCCTCCGAGCAAGATCAGTTCTGGAGAGAGAGAAAGCGCATTAAGCCAGAAATGAGA			4612
Db	481	TCCTCCGAGCAAGATCAGTTCTGGAGAGAGAGAAAGCGCATTAAGCCAGAAATGAGA			540
Qy	4613	ATCTGCGCAGAGGTTTGAAAGCAGCGCCAGAGAGTATGCAAGCTGAGAAAGGGGCCAGT			4672
Db	541	ATCTGCGCAGAGGTTTGAAAGCAGCGCCAGAGAGTATGCAAGCTGAGAAAGGGGCCAGT			600
Qy	4673	GTCCGCCA 4679			
Db	601	GTCCGCCA 607			
RESULT 7					
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LOCUS	AY416721	1515 bp	DNA	linear	GSS 17-DEC-2003
DEFINITION	Homo sapiens MYOC gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY416721				
VERSION	AY416721.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1515)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejalrajal,A.,				
	Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,				
	Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,				
	Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous				
	gene titlos				

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1515)
 AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriter,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.C.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.6e-95;
 Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4120 ATGAGGTTCTTCTGTGACAGTTGCTGAGGCTTGAGATGCAGCTCCAGCTG 4179
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QY 4180 CTGCTTCTGGCTGCTGTGTGGAGTGTGGGAGGAGAGAGAGCTCACTCAGAAAGCC 4239
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 DB 61 CTGCTTCTGGCTGCTGTGTGGAGTGTGGGAGGAGAGAGAGCTCACTCAGAAAGCC 120
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QY 4240 AATGACCAAGTGGCCGATGCGCATATCTTCAAGTGTGGCCAGTCCCAATGAATCAGC 4299
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 DB 121 AATGACCAAGTGGCCGATGCGCATATCTTCAAGTGTGGCCAGTCCCAATGAATCAGC 180
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QY 4300 TGCCAG 4359
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 DB 181 TGCCAG 240
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QY 4360 CAAAGCTTTAGACCTGAGAGGCAAAAGCTGACCTGAGTCCCTGAGAGCTCTCCAC 4419
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 DB 241 CAAAGCTTTAGACCTGAGAGGCAAAAGCTGACCTGAGTCCCTGAGAGCTCTCCAC 300
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QY 4420 CAAATTGACCTTTGACCAAGGCTGCGAGGCGCCAGAGAGAGAGAGAGAGAGAGAG 4479
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 DB 301 CAAATTGACCTTTGACCAAGGCTGCGAGGCGCCAGAGAGAGAGAGAGAGAGAGAG 360
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QY 4480 CTGGGACCTCTGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4539
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QY 4540 GCTTACAGCAACTCTCTCCAGACCAAGTCAAGTTCTGAGAGAGAGAGAGAGAGAG 4599
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 DB 421 GCTTACAGCAACTCTCTCCAGACCAAGTCAAGTTCTGAGAGAGAGAGAGAGAGAG 480
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QY 4600 CAAAGAAAATGAATCTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4659
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QY 4660 AGAAGGGGAG 4719
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 DB 541 AGAAGGGGAG 600
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QY 4720 GAAG 4723
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 DB 601 GAAG 604
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RESULT 8
 BP382502

LOCUS BP382502 608 bp mRNA linear EST 21-SEP-2004
 DEFINITION BP382502 Sugano cDNA library, adipose tissue Homo sapiens cDNA
 clone adsH02027, mRNA sequence.
 ACCESSION BP382502
 VERSION BP382502.1 GI:52418461
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo
 1 (bases 1 to 608)
 Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)

REFERENCE
 15342556
 CONTACT: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="adsH02027"
 /tissue_type="adipose tissue"
 /clone_lib="Sugano cDNA library, adipose tissue"

ORIGIN
 Query Match 10.0%; Score 598.4; DB 3; Length 608;
 Best Local Similarity 99.0%; Pred. No. 1.7e-94;
 Matches 602; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 3964 GCCTACGTGGCACCTCTGTCTTCCCATTAAGAGGCTGCTCCCAATATATTAAC 4023
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QY 4024 CTCTGAGAGCTCAGGATGAGCCAGCAAGGCAACCATCCAGGACCTCTCAGACAGC 4083
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 DB 121 CTCTGAGAGCTCAGGATGAGCCAGCAAGGCAACCATCCAGGACCTCTCAGACAGC 180
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QY 4084 AGAGCTTTCCAGAGAAAGCTTCAACCAAGCTTGCATGAGGTTCTTCTGTGACGTTGC 4143
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 DB 181 AGAGCTTTCCAGAGAAAGCTTCAACCAAGCTTGCATGAGGTTCTTCTGTGACGTTGC 240
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QY 4204 GATGTGGGGGAGAGACAGCTCAGCTCAGAGAGGCCAATGACCAAGTGGCGAGTGCAG 4263
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QY 4384 AAAAGCTGAGCTAGCTCCCTGGAGAGCTCTCCACCAATTGACCTTGGACAGGCTGCC 4443
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 DB 481 AAAAGCTGAGCTAGCTCCCTGGAGAGCTCTCCACCAATTGACCTTGGACAGGCTGCC 540
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QY	4504	GACCAGCT 4511					
Db	601	GACCAGCT 608					
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DEFINITION	56053818H1 FLP Homo sapiens cDNA, mRNA sequence.						
ACCESSION	CD607955						
VERSION	CD607955.1 GI:40256218						
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;						
	Hominidae; Homo.						
REFERENCE	1 (bases 1 to 622)						
AUTHORS	Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.						
TITLE	Circular rapid amplification of cDNA ends for high-throughput						
	extension cloning of partial genes						
	Genomics 84 (1), 205-210 (2004)						
JOURNAL	15203218						
PUBMED	Contact: Fu GK						
COMMENT	Incyte Genomics, Inc.						
	3160 Porter Dr., Palo Alto, CA 94304, USA						
	Tel: 6508454102						
	Email: gfu@incyte.com.						
FEATURES	Location/Qualifiers						
source	1..622						
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QY	4242	TGACCAAGTGGCCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGATCCAGCTG	4301				
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QY	4302	CCCAGAGCAGAGCCCAAGCCATGTCAATCATTAATTACAGAGAGACAGAGACCA	4361				
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.Db		421	GGGCACCTTGAAGGGGGAGCGGGACCGACTGTGGAAACCCAAACCAAGAGATTGGAGACTGC	480
OY		4542	CTACGAGCAACCTCCTCCGAGACAAGTCAATGTTCTTGAGAGAGAAGAAAGCATTAAGSCA	4601
.Db		481	CTACGAGCAACCTCCTCCGAGACAAGTCAATGTTCTTGAGAGAGAAGAAAGCATTAAGSCA	540
OY		4602	AG--AAAATGAAATCTTGCGCCAGAGAGTTGGAANAGACAGCCAGAGAGTAGAAGCTG	4655
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OY		4660	AGAAAGGCCCACTGTCCCCANA	4681
.Db		601	AGAAAGGTGAAGAACCTTCGA	622
RESULT 10				
LOCUS		Bp343359		
DEFINITION		Bp343359 Sugano cDNA library, stomach mucosa Homo sapiens CDNA		
ACCESSION		Bp343359		
VERSION		Bp343359.1 GI:52273246		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo 1 (bases 1 to 583) Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)		
TITLE		Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shiokaneda, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp. Location/Qualifiers		
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source				
ORIGIN				
Query Match		9.7%; Score 583;	DB 3;	Length 583;
Beet Local Similarity		100.0%;	Pred. No. 8.8e-92;	
Matches 583;		Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;
OY		4048	AGCAAGCCACCCATCCAGGACACTCTCAGACAGCAGAGCTTTCAGAGAACTCTAC	4107
.Db		1	AGCAAGCCACCCATCCAGGACACTCTCAGACAGCAGAGACTTTCAGAGAACTCTAC	60
OY		4108	CAAAGCTCTGCAATGAGATTCTTCTGTGACGTTGTCTGACGCTTTGGGCTTGAGATCCA	4167
.Db		61	CAAAGCTCTGCAATGAGATTCTTCTGTGACGTTGTCTGACGCTTTGGGCTTGAGATCCA	120
OY		4168	GCTGTCACGTCGCTGCTTTCGGCTGCTGCTGCTGTGTGGATGTGTGGGGCAGAGACGCTCAG	4227
.Db		121	GCTGTCACGTCGCTGCTTTCGGCTGCTGCTGCTGTGTGGATGTGTGGGGCAGAGACGCTCAG	180
OY		4228	CTCAGAAAGCCATATGACACAGATGGGCGCATGTGCAGATACTTCAGTGTGGCAGCTCCC	4287
.Db		181	CTCAGAAAGCCATATGACACAGATGGGCGCATGTGCAGATACTTCAGTGTGGCAGCTCCC	240
OY		4288	AATGATTCAGCTGCCAGACAGAGCCAGGCCATGTCACTCATTCATTAACAGAGA	4347

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 QY 4408 AGCCTCTCCACCAATTGACCTTGGACAGGCTGCCAGGCCCCAGAGAGCCAGAGAGG 4467
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 QY 4468 CTGCAAGAGGAGCTGGGACACCTGAGAGCCGAGACCAAGTGTGAAACCCAAACCA 4527
 Db 421 CTGCAAGAGGAGCTGGGACACCTGAGAGCCGAGACCAAGTGTGAAACCCAAACCA 480
 QY 4528 GAGTTGAGAGCTGCTTACAGCAACCTCTCCAGACCAAGTGTGAGAGAGAGAG 4587
 Db 481 GAGTTGAGAGCTGCTTACAGCAACCTCTCCAGACCAAGTGTGAGAGAGAGAG 540
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 Db 541 AAGCGACTAAGCGCAAGAAATGAAATCTGGCCAGAGAGTTGG 583

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 LOCUS BP341455 Sugano cDNA library, stomach mucosa Homo sapiens cDNA
 DEFINITION clone STM02509, mRNA sequence.
 ACCESSION BP341455
 VERSION BP341455.1 GI:52271175
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,
 1 (bases 1 to 584)
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
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 /clone_lib="Sugano cDNA library, stomach mucosa"

ORIGIN

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 Matches 583; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 4288 AATGAATCAGTGTGCCAGAGAGCCAGAGCCATGTCAATGATCATTAACAGAGA 4347
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 QY 4408 AGCCTCTCCACCAATTGACCTTGGACAGGCTGCCAGGCCCCAGAGAGCCAGAGAGG 4467
 Db 361 AGCCTCTCCACCAATTGACCTTGGACAGGCTGCCAGGCCCCAGAGAGCCAGAGAGG 420
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 Db 421 CTGCAAGAGGAGCTGGGACACCTGAGAGCCGAGACCAAGTGTGAAACCCAAACCA 480
 QY 4528 GAGTTGAGAGCTGCTTACAGCAACCTCTCCAGACCAAGTGTGAGAGAGAGAG 4587
 Db 481 GAGTTGAGAGCTGCTTACAGCAACCTCTCCAGACCAAGTGTGAGAGAGAGAG 540
 QY 4588 AAGCGACTAAGCGCAAGAAATGAAATCTGGCCAGAGAGTTGGA 4631
 Db 541 AAGCGACTAAGCGCAAGAAATGAAATCTGGCCAGAGAGTTGGA 584

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 ACCESSION CD607956.1 GI:40256219
 VERSION CD607956.1 GI:40256219
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Fu, G.-K., Wang, J. T., Yang, J., Au-Young, J. and Stuve, L. L.
 1 (bases 1 to 617)
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 JOURNAL Genomics 84 (1), 205-210 (2004)
 PUBMED 15203218
 COMMENT Contact: Fu GK
 Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA
 Tel: 6508454102
 Email: gfu@incyte.com.
 Location/Qualifiers
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FEATURES
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 Location/Qualifiers

ORIGIN

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 Best Local Similarity 98.5%; Pred. No. 1.8e-91;
 Matches 597; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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 QY 4122 GAGGTTCTTGTGACAGTTGCTGACAGCTTTGGGCTGAGATGCCAGCTGTCCAGTGT 4181

Db 557 GAGGTTCTTCTGTGACGTTGTCGAGCTTTGGGCTTGAGATCCAGCTGTCCAGCTGCT 498
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Db 18 AAGGTG 13

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DEFINITION HRT09556, mRNA sequence.
ACCESSION BP260344
VERSION BP260344.1 GI:52175575
KEYWORDS EST.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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ORIGIN

Query Match 9.7%; Score 581; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4103 CTCACCAAGCTCTGCAATGAGGTTCTTGTGTGACGTTGTCAGCTTTGGGCTTGA 4162
Db 61 CTCACCAAGCTCTGCAATGAGGTTCTTGTGTGACGTTGTCAGCTTTGGGCTTGA 120
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Db 181 CTCAGCTCAGAAAGCCATGACAGAGTGGCCGATGCACTATACCTTCAGTGTGCA 240
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DEFINITION BP342027
ACCESSION BP342027
VERSION BP342027.1 GI:52271793
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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GenCore version 5.1.7
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(without alignments)
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Searched: 1303057 seqs, 888780828 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	4015.8	66.9	5271	3	US-09-306-828-34
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9	2773.4	46.2	2800	3	US-10-017-870-10
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38	519.6	8.7	1491	6	PCT-US95-1402A-3	Sequence 3, App11
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42	225.4	3.8	2232	3	US-09-306-828-38	Sequence 38, App11
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ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF GLAUCOMA AND
; TITLE OF INVENTION: RELATED DISEASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,669A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/791,154
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mendelson, Elliot
; REGISTRATION NUMBER: P-42,878
; REFERENCE/DOCKET NUMBER: 07425-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-6857
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-938-669A-3
Query Match 81.5%; Score 4888.8; DB 3; Length 6169;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;

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QY 1261 GCTTCAAGTCCAGAGAAATTCAGAGAGTGGGAGCTGCAGAGAGTGGGAGCGCTGGGGC 1320
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QY 1321 TGAAGGGGTGCTGAAGGAGGAAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAGATGTC 1380
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QY 1381 AGTGTGTTTCAAGGGGCTGGAGTTCCTGTTGCTCTGTGAGAGCTTTTATCTTTCT 1440
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QY 1441 CTGCTTGAAGGAGAAAGATCTAATTCATGAAGGGAATGCAATTCATTAAGTCACTGTT 1500
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QY 2161 TGACAGACCCCGCAGCTCAGAGTGACTGCTGACAGCAGGAGTGACTGACAGGC 2220
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QY 2221 AGGGAG 2280
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QY 2281 GGCAGTGGGAATTGACCAAGAGATTAATGACAGTATCTGAGGTTCTAGAGAGGAGG 2340
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RESULT 2
US-09-306-828-3
/ Sequence 3, Application US/09306828
/ Patent No. 6475724
/ GENERAL INFORMATION:
/ APPLICANT: Nguyen, Thai D.
/ APPLICANT: Polansky, Jon R.
/ APPLICANT: Chen, Pu
/ APPLICANT: Chen, Hua
/ TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
/ CURRENT APPLICATION NUMBER: US/09/306,828
/ EARLIER FILING DATE: 1999-05-07
/ EARLIER APPLICATION NUMBER: US 09/227,881
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: Microsoft Word 97
/ SEQ ID NO 3
/ LENGTH: 6169
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-306-828-3

Query Match 81.5%; Score 4888.8; DB 3; Length 6169;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;

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QY 61 CGTAGAGGTGAGGGTCTGTGTCTTACACCTTACCTGTATGTCTTACACCTGAGCTCACTGC 120
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QY 1081 CTTTCAAGCTCTCTCTCAATGTCACAGGCTGAGCTGGCTGCTGCTGCTGCTGCTGCTG 1140
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QY	1201	AGAGGAAACTAGTCTAAACGAGAACTGAGAGGGGACAGTGTTTCTCAGAGCGAAAGG	1260
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QY	1261	GCCTCCAGTCCAGAGAAATTCAGAGAGTGGGACCTCAGGAGTGGGACGCTGGGGC	1320
Db	2476	GCCTCCAGTCCAGAGAAATTCAGAGAGTGGGACCTCAGGAGTGGGACGCTGGGGC	2535
QY	1321	TGAGCGGCTGCTGAAAGGCAAGAGGTGAAAAGGCAAGCTGAAGCTGCCAAGATGTC	1380
Db	2536	TGAGCGGCTGCTGAAAGGCAAGAGGTGAAAAGGCAAGCTGAAGCTGCCAAGATGTC	2595
QY	1381	AGTGTGTTCAAGGGGCTGGAGTTTCCGTTGCTTCTGAGAGCTTTTATCTTTTCT	1440
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QY	1441	CTGCTTGAGAGAGAAAGTCTAATTCATGAAGGATGCACTTTCATTAAGTCAAGCTGT	1500
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QY	1681	AACTTGAAATCAGAGACCTGGGTTTTCTTCTGATCTGCAATTGTTGGCTGTGGAC	1740
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QY	1801	GCTCTCGTGTCTGTGAACCTTCCCTGTGATTCCTCTGAGGGGGAGTGTGAGAGGG	1860
Db	3016	GCTCTCGTGTCTGTGAACCTTCCCTGTGATTCCTCTGAGGGGGAGTGTGAGAGGG	3075
QY	1861	AAGAGGCAAGCTGGAGCAGCTGAGCCACAGGGAGGTGAGGGGACAGAAAGCAGG	1920
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QY	1921	CAGAAAGCTGGGTGCTCACTAGTCTCTCACTGATCAGTCACTCCAGACCCAGAGCCA	1980
Db	3136	CAGAAAGCTGGGTGCTCACTAGTCTCTCACTGATCAGTCACTCCAGACCCAGAGCCA	3195
QY	1981	CAATGCTTCAGAAAAGCTCAATGAACCCACAGCAATTTTCCCTCCCTAAGATATGAC	2040
Db	3196	CAATGCTTCAGAAAAGCTCAATGAACCCACAGCAATTTTCCCTCCCTAAGATATGAC	3255
QY	2041	AATGCAATTTGCCAATTAACAAAAAGATGACAGACTAACTGGTGTAGCTTTTGCTG	2100
Db	3256	AATGCAATTTGCCAATTAACAAAAAGATGACAGACTAACTGGTGTAGCTTTTGCTG	3315
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Db	3316	GCATTTCAAAACTGGGCCAGAGCAAGTGAATAATGCAAGATTTGTTAACTTTTCAACC	3375
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Db	3376	TGACCAAGCAACCCACGACGCTCAGACATGACTGTGACACACAGGAATGACCTGACGCG	3435
QY	2221	AGGGAGAGAGAAAAAGAGGGGATATGTGTATGACAAAGAAAGACAGATTAATTCAG	2280

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Qy	2341	GCTATATTGTGGGGGAAAAATCATGTTCAAGGAAAGTCGGAGACTGATTTCTATAC	2400
Db	3556	GCTATATTGTGGGGGAAAAATCATGTTCAAGGAAAGTCGGAGACTGATTTCTATAC	3615
Qy	2401	TATATTTTCCTTTACAAGCTGAGTAATCTGACCAAGTCAAGGTATAGTAACTGAGCT	2460
Db	3616	TATATTTTCCTTTACAAGCTGAGTAATCTGACCAAGTCAAGGTATAGTAACTGAGCT	3675
Qy	2461	GTTAAGTTACTAGTTGTCTCCATTATAGGAAGCTCTTTTCTGTGAGTTAGCAGACA	2520
Db	3676	GTTAAGTTACTAGTTGTCTCCATTATAGGAAGCTCTTTTCTGTGAGTTAGCAGACA	3735
Qy	2521	AGGGCAATCCGGTTCTTTTAAAGAAAGAAACATTCCTAAGATAAGCCAAACAGAT	2580
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Qy	2581	TCAAGCCTAGGTTCTTGCGTACTATATGATTTGGTATTTTGAAAAATCATTCAGGATGT	2640
Db	3796	TCAAGCCTAGGTTCTTGCGTACTATATGATTTGGTATTTTGAAAAATCATTCAGGATGT	3855
Qy	2641	TACTATCTGATTCAGAAAATGAGCTGATGACCTTGGTCAAGCTGTAACAAACCAT	2700
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Qy	2880	CATTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGGTATATTATTTGGCTATTCG	2939
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Qy	3000	CAGTCCAGAAACCTGAGAAATTGAAAGAGAAAAATTAATCATTTTGTGTTTACACCT	3059
Db	4215	CAGTCCAGAAACCTGAGAAATTGAAAGAGAAAAATTAATCATTTTGTGTTTACACCT	4274
Qy	3060	TCTAATCAAAATTTAAATTTTATTCATTTGCAATGAGCATTAAGCTCAAGGTGTAAT	3119
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Qy	3120	AACAGTACTGTGTATTTTGTCAATTAACAATAGAAATCAAGATTTTATCTATATTAC	3179
Db	4335	AACAGTACTGTGTATTTTGTCAATTAACAATAGAAATCAAGATTTTATCTATATTAC	4394
Qy	3180	AGTTGTGCGAATACGTTGTAGTGAATTTTATATCTAAAACTACTTTGAAATTAGAC	3239
Db	4395	AGTTGTGCGAATACGTTGTAGTGAATTTTATATCTAAAACTACTTTGAAATTAGAC	4454
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RESULT 3
 US-08-938-669A-1
 / Sequence 1, Application US/08938669A
 / Patent No. 6171788
 / GENERAL INFORMATION:
 / APPLICANT: Nguyen, Thai D.
 / APPLICANT: Polansky, Jon R.
 / TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
 / TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
 / NUMBER OF SEQUENCES: 32
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Howrey & Simon
 / STREET: 1299 Pennsylvania Avenue, N.W.
 / CITY: Washington
 / STATE: DC
 / COUNTRY: USA
 / ZIP: 20004-2402
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: PASEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/938,669A
 / FILING DATE:
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/791,154
 / FILING DATE: 28-JAN-1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Mendelson, Elliot
 / REGISTRATION NUMBER: P-42,878
 / REFERENCE/DOCKET NUMBER: 07425-0034
 / TELECOMMUNICATION INFORMATION:

;
 ; TELEPHONE: 202 383-6857
 ; TELEFAX: 202 383-6610
 ;
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5300 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ;
 ; US-08-938-669A-1

Query Match 67.8%; Score 4069.4; DB 3; Length 5300;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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QY      61 CGTAGAGGTGAGGGTCTGTCTTACACCTACCTGATGCTCTACACCTGAGCTCACTGC 120
DB      1276 CGTAGAGGTGAGGGTCTGTCTTACACCTACCTGATGCTCTACACCTGAGCTCACTGC 1335
QY      121 AACCTCTGCTCCAGGTTCAAGCAATTCCTCTCTCAGCCTCCCGCGTAGCTGGAGCT 180
DB      1336 AACCTCTGCTCCAGGTTCAAGCAATTCCTCTCTCAGCCTCCCGCGTAGCTGGAGCT 1395
QY      181 AAGAGGCGACGCCCGGCTAATTTTGTATTTAGTAGAGATGGGGTTTACCATATTAG 240
DB      1396 AAGAGGCGACGCCCGGCTAATTTTGTATTTAGTAGAGATGGGGTTTACCATATTAG 1455
QY      241 CCCGGGTGCTTGAACCTCTGACCTCAGATGATCCACCACCTGACCTCCCTAAAGTGC 300
DB      1456 CCCGGGTGCTTGAACCTCTGACCTCAGATGATCCACCACCTGACCTCCCTAAAGTGC 1515
QY      301 TGGGATTACAGGATGATGACCGCGCGCCGCGCAAGGGTCACTGTTTAATAGAAATAC 360
DB      1516 TGGGATTACAGGATGATGACCGCGCGCCGCGCAAGGGTCACTGTTTAATAGAAATAC 1575
QY      361 TTGAATGGTTTACTAAACCAACAGGAAACAGACAAAGCTGTGATATTTTCAAGGATTC 420
DB      1576 TTGAATGGTTTACTAAACCAACAGGAAACAGACAAAGCTGTGATATTTTCAAGGATTC 1635
QY      421 TTGGATGGGGAATGGTGCATGAGCTGCTGCTAGTCCAGACCACTGCTCATATCA 480
DB      1636 TTGGATGGGGAATGGTGCATGAGCTGCTGCTAGTCCAGACCACTGCTCATATCA 1695
QY      481 CTTTCTTCCCTCATCTCAATTTTCAAGGCTAAGTTACATTTTATTTTCAACATCTTTTGTG 540
DB      1696 CTTTCTTCCCTCATCTCAATTTTCAAGGCTAAGTTACATTTTATTTTCAACATCTTTTGTG 1755
QY      541 GTAAACCTTCCATGTTACTGAATTAAGATATACATTAACCTAATTTTGGGGCCA 600
DB      1756 GTAAACCTTCCATGTTACTGAATTAAGATATACATTAACCTAATTTTGGGGCCA 1815
QY      601 TCTGTGTGTGTATATAGGGGAGAGGGGCAATCCCAAGAGACTCTTTGAAGCCCGGGCAG 660
DB      1816 TCTGTGTGTGTATATAGGGGAGAGGGGCAATCCCAAGAGACTCTTTGAAGCCCGGGCAG 1875
QY      661 AGGTTTCTCTCAGCTGGGGAGGCTTGCAAGACCCGGGGTCTGTGGTGTCTGAGCA 720
DB      1876 AGGTTTCTCTCAGCTGGGGAGGCTTGCAAGACCCGGGGTCTGTGGTGTCTGAGCA 1935
QY      721 ACCTCGAGCCCGGTGCCACTGTTGTGTTTGTATCACTCTCTAGAGGACTGTGCTTTCT 780
DB      1936 ACCTCGAGCCCGGTGCCACTGTTGTGTTTGTATCACTCTCTAGAGGACTGTGCTTTCT 1995
QY      781 ATTCTGTGTGACTGTTCAATTCATCAGGCAATTCATTGACAAATTTATTTAGTACTTATA 840
DB      1996 ATTCTGTGTGACTGTTCAATTCATCAGGCAATTCATTGACAAATTTATTTAGTACTTATA 2055
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QY      961 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGATTGTGCGAGCACTCCCTTAACAA 1020
DB      2176 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGATTGTGCGAGCACTCCCTTAACAA 2235
QY      1021 GGCACCTCTTAGGCCCCCTGCTGCTCATCTGTCGCCGAGGAGCCCAAGCCGAGT 1080
DB      2236 GGCACCTCTTAGGCCCCCTGCTGCTCATCTGTCGCCGAGGAGCCCAAGCCGAGT 2295
QY      1081 CTTCCAGCTCTCTCTCTCATATGTCACAGCGCTGACAGTGGCTGCTGCTTCCCTGT 1140
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QY      1141 AATGCTCTGCTGATCTGAGCTGGAGA CTCTTGGCTCCAGGCTCCAGAAAGAAATAG 1200
DB      2356 AATGCTCTGCTGATCTGAGCTGGAGACTCTTGGCTCCAGGCTCCAGAAAGAAATAG 2415
QY      1201 AAGAGGAAACTAGTCTAAACGAGAACTGAGAGGGACAGTGTTCCTCAGAGGAAAGGG 1260
DB      2416 AAGAGGAAACTAGTCTAAACGAGAACTGAGAGGGACAGTGTTCCTCAGAGGAAAGGG 2475
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 QY 4079 ACAGC 4083
 Db 5296 ACAGC 5300


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RESULT 4
US-09-306-828-1
; Sequence 1, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-1

Query Match      67.8%; Score 4069.4; DB 3; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY      1 GCTCCACAGGAAGTCTCCCACTGATGACTTTCGATCAGATGTTACAGCCAGAAAGTTC 60
DB      1216 GCTCCACAGGAAGTCTCCCACTGATGACTTTCGATCAGATGTTACAGCCAGAAAGTTC 1275
QY      61 CGTAGAGGTGAGGGTCTGTGTCTTACACCTACCTGATGCTCTACACCTGAGCTCATGCG 120
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DB      1576 TTGAATGTTTACTAATCAACACAGGAAACAGCAAAAGCTGTGATTAATTCAGGATTC 1635
QY      421 TTGGATGAGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB      1636 TTGGATGAGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1695
QY      481 GTTCTTCTCTCATCTCTCATCTCTCATCTCTCATCTCTCATCTCTCATCTCTCTTTTGTG 540
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QY      541 GTTAAGCTTCACATCTCTTACTAATAAATTAAGATTAATAAATTAAGTTCATTTTGGGCGCA 600
DB      1756 GTTAAGCTTCACATCTCTTACTAATAAATTAAGATTAATAAATTAAGTTCATTTTGGGCGCA 1815
QY      601 TCTGTGTGTGTGTATAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB      1816 TCTGTGTGTGTGTATAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1875
QY      661 AAGTTTCTCTCTCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB      1876 AAGTTTCTCTCTCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1935
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QY      721 ACCTGCGAGCGCGTGCACATGATGTTTGTATATCATCTGTAAGGACCTGTGCTTCT 780
DB      1936 ACCTGCGAGCGCGTGCACATGATGTTTGTATATCATCTGTAAGGACCTGTGCTTCT 1995
QY      781 ATTTCTGTGTGACTCGTTCATTCATTCAGGACATTCATGACATTTATTTAGAGTATATA 840
DB      1996 ATTTCTGTGTGACTCGTTCATTCATTCAGGACATTCATGACATTTATTTAGAGTATATA 2055
QY      841 TCTGCCAGACACCAAGACAAATATGTTGACAAAGCATGACTGCTTACCTTGTGAG 900
DB      2056 TCTGCCAGACACCAAGACAAATATGTTGACAAAGCATGACTGCTTACCTTGTGAG 2115
QY      901 GTGACAGTTTCTCATAGGAAGAGTGCAGAGAAATTAATTAACCGACCACTTAACCA 960
DB      2116 GTGACAGTTTCTCATAGGAAGAGTGCAGAGAAATTAATTAACCGACCACTTAACCA 2175
QY      961 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGATTTGTCGAGCATTCCTTAACA 1020
DB      2176 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGATTTGTCGAGCATTCCTTAACA 2235
QY      1021 GGCACATCTCCTAGCGCCCTGCTGCTCATCTGTCGAGAGGCCCAAGCCGAGT 1080
DB      2236 GGCACATCTCCTAGCGCCCTGCTGCTCATCTGTCGAGAGGCCCAAGCCGAGT 2295
QY      1081 CTTCACAGCTCTCTCTCATATGATCAGAGCCTGAGTGGCTGCTGCTTCCCTG 1140
DB      2296 CTTCACAGCTCTCTCTCATATGATCAGAGCCTGAGTGGCTGCTGCTTCCCTG 2355
QY      1141 AATCGCTCTGTGATCTGAGCTGAGAGTCTCTTGGCTCAGGCTCAGAAAGAAATAG 1200
DB      2356 AATCGCTCTGTGATCTGAGCTGAGAGTCTCTTGGCTCAGGCTCAGAAAGAAATAG 2415
QY      1201 AAGAGGAAATAGTCTTAACGAGAAATCTGAGAGGAGCAGTGTCTTCTCAGAGGAAAGAG 1260
DB      2416 AAGAGGAAATAGTCTTAACGAGAAATCTGAGAGGAGCAGTGTCTTCTCAGAGGAAAGAG 2475
QY      1261 GCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGACAGGAGTGGGAGAGCTGGGAG 1320
DB      2476 GCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGACAGGAGTGGGAGAGCTGGGAG 2535
QY      1321 TGAGCGGGTGTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
DB      2536 TGAGCGGGTGTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2595
QY      1381 AGTGTGTTCACGAGGAGTGGAGGAGTTCGTTGCTTCTGTGAGCCTTTTATCTTTTCT 1440
DB      2596 AGTGTGTTCACGAGGAGTGGAGGAGTTCGTTGCTTCTGTGAGCCTTTTATCTTTTCT 2655
QY      1441 CTGCTTGAAGAGAAAGAGTCTATTCATGAAGGAGTCACTTTCATTAAGTCACTGTT 1500
DB      2656 CTGCTTGAAGAGAAAGAGTCTATTCATGAAGGAGTCACTTTCATTAAGTCACTGTT 2715
QY      1501 AAAATTCAGAGGAGTGCATGAGGTTTCTCTCAGAGAGCCTTATTAATGGAATATAG 1560
DB      2716 AAAATTCAGAGGAGTGCATGAGGTTTCTCTCAGAGAGCCTTATTAATGGAATATAG 2775
QY      1561 GAAAGGAGCTCATTTCTAGGCGCTTAATTCACGAGAAAGTCACTGAGTCTTTCTTT 1620
DB      2776 GAAAGGAGCTCATTTCTAGGCGCTTAATTCACGAGAAAGTCACTGAGTCTTTCTTT 2835
QY      1621 CATGTCTTCTGGGCAACTACTACGCTCTGTGTGAGCTTGGCTTATGCAAGCGTCA 1680
DB      2836 CATGTCTTCTGGGCAACTACTACGCTCTGTGTGAGCTTGGCTTATGCAAGCGTCA 2895
QY      1681 AACCTTGAAATCAGAGACTCGGTTTCTTTCTGAGTTCGACATGTTGCTGAGGAG 1740
DB      2896 AACCTTGAAATCAGAGACTCGGTTTCTTTCTGAGTTCGACATGTTGCTGAGGAG 2955
QY      1741 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGCTTCTCTGCTAATAAGACCTTTC 1800
DB      2956 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGCTTCTCTGCTAATAAGACCTTTC 3015
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QY	1801	GCTCTCGTGTTCGTGAAACA	CTTCCCTGTGATTTCTCTGTGAGGGGGGA	TTCTTGAAGAGGG	1860
Db	3016	GCTCTCGTGTTCGTGAAACA	CTTCCCTGTGATTTCTCTGTGAGGGGGGA	TTCTTGAAGAGGG	3075
QY	1861	AAGGAGCGAGAGCTGAGAGCA	GCTGAGCAACAAGGGGAGGTGAGGGGGGACAGAAAGCAGG	1920	
Db	3076	AAGGAGCGAGAGCTGAGAGCA	GCTGAGCAACAAGGGGAGGTGAGGGGGGACAGAAAGCAGG	3135	
QY	1921	CAGAAGCTGGGTGCTCAATCA	GTCTGACTGATCAGTCAAGCTCAGACCTCAGAACCCAGAGCCA	1980	
Db	3136	CAGAAGCTGGGTGCTCAATCA	GTCTGACTGATCAGTCAAGCTCAGACCTCAGAACCCAGAGCCA	3195	
QY	1981	CAATGCTTCAGAAAAGCTCA	ATGAAACCAACAGCCAATTTTCTTCCCTTAAGATAGAC	2040	
Db	3196	CAATGCTTCAGAAAAGCTCA	ATGAAACCAACAGCCAATTTTCTTCCCTTAAGATAGAC	3255	
QY	2041	AATGGCAATTTGSCAATATAC	CAAAAAAGATGACAGAGCAATACGAGTGGTAGCTTTGGCTG	2100	
Db	3256	AATGGCAATTTGSCAATATAC	CAAAAAAGATGACAGAGCAATACGAGTGGTAGCTTTGGCTG	3315	
QY	2101	GCATTTCAAAACTGGGCG	CAGAGCAAGTGGAAAAATGCGAGATTTGTTAACTTTTCAACC	2160	
Db	3316	GCATTTCAAAACTGGGCG	CAGAGCAAGTGGAAAAATGCGAGATTTGTTAACTTTTCAACC	3375	
QY	2161	TGACACGACCCCAACGAC	GCTCAGCTGCTGACAGACGGAATGACCTGACAGCG	2220	
Db	3376	TGACACGACCCCAACGAC	GCTCAGCTGCTGACAGACGGAATGACCTGACAGCG	3435	
QY	2221	AGGGGAGGAGAAAAAAGAG	AGGAGGTAGTGTATAGACAGAAAGACAGATTCATTCAAG	2280	
Db	3436	AGGGGAGGAGAAAAAAGAG	AGGAGGTAGTGTATAGACAGAAAGACAGATTCATTCAAG	3495	
QY	2281	GGCAGTGGAAATTGACAC	ACAGGATTTATAGTCCACGTGATCTGGGTTCTAGAGGACG	2340	
Db	3496	GGCAGTGGAAATTGACAC	ACAGGATTTATAGTCCACGTGATCTGGGTTCTAGAGGACG	3555	
QY	2341	GCTATATTGTGGGGGAAAAA	ATCATGTTCAAGGGAAGTCCGGGACACTGATTTCTAATAC	2400	
Db	3556	GCTATATTGTGGGGGAAAAA	ATCATGTTCAAGGGAAGTCCGGGACACTGATTTCTAATAC	3615	
QY	2401	TATATTTTCTTTACAGCT	GAGTAATTTGAGCAAGTCACAAGGTATGTAACGAGGCT	2460	
Db	3616	TATATTTTCTTTACAGCT	GAGTAATTTGAGCAAGTCACAAGGTATGTAACGAGGCT	3675	
QY	2461	GTAAGATTACTTAGTTTCT	CTCTTAATAGAACTCTTTTCTCTGTGAGTTAGACACA	2520	
Db	3676	GTAAGATTACTTAGTTTCT	CTCTTAATAGAACTCTTTTCTCTGTGAGTTAGACACA	3735	
QY	2521	AGGGCAATCCCGTTCT	TTTATACAGAAAGAAAACATTCCTAAGAGTAAGCCAAACAGAT	2580	
Db	3736	AGGGCAATCCCGTTCT	TTTATACAGAAAGAAAACATTCCTAAGAGTAAGCCAAACAGAT	3795	
QY	2581	TCAAGCCTTAGTCTTGCT	GACTATATATGATTTTGTGAAAATCATTTTACAGGAGTT	2640	
Db	3796	TCAAGCCTTAGTCTTGCT	GACTATATATGATTTTGTGAAAATCATTTTACAGGAGTT	3855	
QY	2641	TACTATCTGATTCAGAAA	ATGAGACTAGTACCCTTGGTCAAGCTGTAAACAAACCCAT	2700	
Db	3856	TACTATCTGATTCAGAAA	ATGAGACTAGTACCCTTGGTCAAGCTGTAAACAAACCCAT	3915	
QY	2701	TTGTAAATGTCTCAAGT	TCAGGCTTAACTCAGAACCAATCAATTAAGATAGATCTTT	2760	
Db	3916	TTGTAAATGTCTCAAGT	TCAGGCTTAACTCAGAACCAATCAATTAAGATAGATCTTT	3975	
QY	2761	AGAGCAAACTGTGTTTCT	CAACTCTGAGAGTGAAGTCCAGGGGACGTTTGAAATATTT	2820	
Db	3976	AGAGCAAACTGTGTTTCT	CAACTCTGAGAGTGAAGTCCAGGGGACGTTTGAAATATTT	4035	
QY	2821	ACTTCACAAGTATGAC	ACTGTGTTGTTGATTAACAACATTAAGTTGCTCAAGAGCAATC	2880	
Db	4036	ACTTCACAAGTATGAC	ACTGTGTTGTTGATTAACAACATTAAGTTGCTCAAGAGCAATC	4095	
QY	2881	ATTATATTCAGTGGCT	TAAAGTTACTCTGACAGTTTGGTATATTTATGGCTATTGCC	2940	

Db	4096	ATTATTTTCAAGTGGCTTAAAGTTACTTCAAGCTTTTGGTATATTATTTAGGCAATTGGC	4155
Qy	2941	ATTTCGTTTTTGTGTTTTCTCTTTGGGTTATTATATGTAAAGCAGGATTTTAACCTAC	3000
Db	4156	ATTTCGTTTTTGTGTTTTCTCTTTGGGTTATTATATGTAAAGCAGGATTTTAACCTAC	4215
Qy	3001	AGTCCAGAAAAGCCGTGTAATTGGAATGAGAAAAAATTAACATTTTGTGTTTTACCACTT	3060
Db	4216	AGTCCAGAAAAGCCGTGTAATTGGAATGAGAAAAAATTAACATTTTGTGTTTTACCACTT	4275
Qy	3061	CTAACTAAATTTACATTTTATTTATTCATTGGCAATAGACCATAAATCTCAAGTGTATATA	3120
Db	4276	CTAACTAAATTTACATTTTATTTATTCATTGGCAATAGACCATAAATCTCAAGTGTATATA	4335
Qy	3121	ACAGTACCTGTGATTTTGTCTATTAACCAATGAAAATCAAGACATTTTATATCTATATTACA	3180
Db	4336	ACAGTACCTGTGATTTTGTCTATTAACCAATGAAAATCAAGACATTTTATATCTATATTACA	4395
Qy	3181	GTGTGTGCAGATACGTTGTGTAAAGTAATTTTATATCTCAAAACATCTTTGAAAATTAAAC	3240
Db	4396	GTGTGTGCAGATACGTTGTGTAAAGTAATTTTATATCTCAAAACATCTTTGAAAATTAAAC	4455
Qy	3241	TCCGCTGGAGATCTTGTTTTTAAACATTAATTAACAAAGTTTAAATTTTGAATTTTGA	3300
Db	4456	TCCGCTGGAGATCTTGTTTTTAAACATTAATTAACAAAGTTTAAATTTTGAATTTTGA	4515
Qy	3301	TAACTATATTTTCATTATCATTTTGTGTTTCCCTTGTATCTATATTTTATATTTGAAAACA	3360
Db	4516	TAACTATATTTTCATTATCATTTTGTGTTTCCCTTGTATCTATATTTTATATTTGAAAACA	4575
Qy	3361	TCTTTCTGAGAAGAGTTCCCCAGATTTTCCCAATGAGAGTTCTTGGCATGCAACAACAG	3420
Db	4576	TCTTTCTGAGAAGAGTTCCCCAGATTTTCCCAATGAGAGTTCTTGGCATGCAACAACAG	4635
Qy	3421	AGTAGAAGCTGATTTTGAAGAGCTTAACATTTGACATTTGGTGCCTGAGATGCAAGACTGAATT	3480
Db	4636	AGTAGAAGCTGATTTTGAAGAGCTTAACATTTGACATTTGGTGCCTGAGATGCAAGACTGAATT	4695
Qy	3481	AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAAGGGGTGAAGGGGAAAATCTGC	3540
Db	4696	AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAAGGGGTGAAGGGGAAAATCTGC	4755
Qy	3541	CGCTTCTTAAAGAAATGCTCTCCCTGAGAGCCGTGTAGGGGTGCTGTCTTGTGTCTGCGTG	3600
Db	4756	CGCTTCTTAAAGAAATGCTCTCCCTGAGAGCCGTGTAGGGGTGCTGTCTTGTGTCTGCGTG	4815
Qy	3601	GCTGTATATTTTCTCTGTCCCTGCTCAAGCTTAAGAGACTTGTTTGAATCTCCAGTTCCT	3660
Db	4816	GCTGTATATTTTCTCTGTCCCTGCTCAAGCTTAAGAGACTTGTTTGAATCTCCAGTTCCT	4875
Qy	3661	AGCATATGAGCTGAGCAGATGCAAGTTCTCATATGAGTTTGCAGATGTAATGGAATAATATA	3720
Db	4876	AGCATATGAGCTGAGCAGATGCAAGTTCTCATATGAGTTTGCAGATGTAATGGAATAATATA	4935
Qy	3721	ACTAGAAAATATATCTTGTGTAAATCAGACACACAGTATGCTCGTGTAAGTGTGTATC	3780
Db	4936	ACTAGAAAATATATCTTGTGTAAATCAGACACACAGTATGCTCGTGTAAGTGTGTATC	4995
Qy	3781	--GT	3838
Db	4996	GT	5055
Qy	3839	GGGTATGGGTGATCAATTAATTGGATGTTCTTTTAAAGAAATCTCAACAGACTTCTGG	3896
Db	5056	GGGTATGGGTGATCAATTAATTGGATGTTCTTTTAAAGAAATCTCAACAGACTTCTGG	5115
Qy	3899	AAGTTATATTTTCTAAGAAATCTTGCTGAGCAGGTGAAGGCAACCCCTGTGACAGCCCC	3956
Db	5116	AAGTTATATTTTCTAAGAAATCTTGCTGAGCAGGTGAAGGCAACCCCTGTGACAGCCCC	5175
Qy	3959	ACCCAGCTCACGTGGCCACTGTGTCTTCCCAATGAAGGCTGTGCTCCCAAGTATATA	4018

Db	5176	ACCAGGCTCAGNNGGCACCTCTGTCTTCTCCCCATGAAGGGCTGGCTCCCAAGATATA	5235
Oy	4019	TAAACCTCTCGAGCTCAGGCATGAGGCACCAAGGCCACCATTCAGGCACTTCAGC	4078
Db	5226	TAAACCTCTCTGGAGCTCGGGCATGAGCCAGGCCACCATTCAGGCACTTCAGC	5295
Oy	4079	ACAGC 4083	
Db	5296	ACAGC 5300	

RESULT 5
US-08-938-669A-2

Sequence 2, Application US/08938669A
Patent No. 617178
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
METHODS OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESS: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA

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;      ZIP:  20004-2402
;      COMPUTER READABLE
;

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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: OPERATING SYSTEM: DOS
: SOFTWARE: FastSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:

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COMMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot

REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
FBI DOCUMENTATION: INFORMATION

TELECOMMUNICATION INFORMATION
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610

TELEPHONE. 202 363-0810
TELEX:
INFORMATION FOR SEO ID NO: 2.

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 5304 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single

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TOPLOGY:
US-08-938-669A-2

Query Match	67.6%	Score 4057.4;	DB 3;	Length 5304;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 4077;	Conservative	0;	Mismatches 6;	Indels 6;
				Gaps 1.

QY	1	GCTTCACAGGAAGTCTCCCACTAGACTTCTGCATCAACATGTTAAGCCAGAAAGTTC	60
Db	1216	GCTTCACAGGAAGTCTCCCACTAGACTTCTGCATCAACATGTTAAGCCAGAAAGTTC	1275
QY	61	CGTAGAGGTGAAGGTTCTGTGTTCTTACACTTACCTGTATGCTCTTACACCTGAAGCTCACTGC	120
Db	1276	CGTAGAGGTGAAGGTTCTGTGTTCTTACACTTACCTGTATGCTCTTACACCTGAAGCTCACTGC	1335
QY	121	AACTCTGACCTCCCAAGGTTCAAGAAATTCCTCTCTCAAGCTCCCGGTATGCTGGAACT	180
Db	1336	AACTCTGACCTCCCAAGGTTCAAGAAATTCCTCTCTCAAGCTCCCGGTATGCTGGAACT	1395

OY	181	ACAGGCGACGCGCGGCTAATTTTGTATGTGTGTAGAGATGGGGTTTCCACATATAG	240
Db	1336	ACGGCGCACGCGCGGCTAATTTTGTATGTGTGTAGAGATGGGGTTTCCACATATAG	1455
OY	241	CCCGGCTGGTCTTGAACCTCTGACCTCAGGTGATCAACCACCTCAGCCTCCTAAGATGC	300
Db	1456	CCCGGCTGGTCTTGAACCTCTGACCTCAGGTGATCAACCACCTCAGCCTCCTAAGATGC	1511
OY	301	TGGGATTAACGGCATGAGTCAACCGGCGCGGCCCAAGGGTCAAGTGTATTAAGAAATAAC	360
Db	1516	TGGGATTAACGGCATGAGTCAACCGGCGCGGCCCAAGGGTCAAGTGTATTAAGAAATAAC	1576
OY	361	TTGAATGTGTTTACTTAACCAACAGGGAACAAGACAAAGCTGTGATATTTTCAAGGATTC	420
Db	1576	TTGAATGTGTTTACTTAACCAACAGGGAACAAGACAAAGCTGTGATATTTTCAAGGATTC	1635
OY	421	TTGGGATGGGGAATGGTGCATGTAGAGCTCCGCGCTAGTCCGACACATCGGTCCTCATCA	480
Db	1636	TTGGGATGGGGAATGGTGCATGTAGAGCTCCGCGCTAGTCCGACACATCGGTCCTCATCA	1695
OY	481	CTTTCTTCCTCATCTCATTTTCAAGGCTAAGTTACCAATTTATTTCAACATGCTTTTGTG	540
Db	1696	CTTTCTTCCTCATCTCATTTTCAAGGCTAAGTTACCAATTTATTTCAACATGCTTTTGTG	1755
OY	541	GTAAGCCTCCACATCTGTTACTGAAATTAAGATATACATAACCTAGTTCATTTGGGCGCA	600
Db	1756	GTAAGCCTCCACATCTGTTACTGAAATTAAGATATACATAACCTAGTTCATTTGGGCGCA	1815
OY	601	TCGTGTGTGTGTATAGGGGAGAGGGGATACCCACAGACCTCCGTGAAGCCCCGGGAG	660
Db	1816	TCGTGTGTGTGTATAGGGGAGAGGGGATACCCACAGACTCTCTGAAGCCCCGGGAG	1875
OY	661	AGGTTTCTCTCCAGCTGGGGGAGCCCTGCAGACACCGGGGTCTGTGGTCTCTGAGCA	720
Db	1876	AGGTTTCTCTCCAGCTGGGGGAGCCCTGCAGACACCGGGGTCTGTGGTCTCTGAGCA	1935
OY	721	ACCTGCCAGCCCGTGCCACTGTGTTGTTTGTATATCATCTTAGAGACCTGTGCTTCT	780
Db	1936	ACCTGCCAGCCCGTGCCACTGTGTTGTTTGTATATCATCTTAGAGACCTGTGCTTCT	1995
OY	781	ATTCTGTGTGTACGTGTTCAATTCACAGGATTCATTTGCAATTTATGTAGTACTTATA	840
Db	1996	ATTCTGTGTGTACGTGTTCAATTCACAGGATTCATTTGCAATTTATGTAGTACTTATA	2055
OY	841	TCTGCCAGACACACAGAGCAAAATGTGTAGCAAGCATCATGCCCTACCTTGCTGAGAG	900
Db	2056	TCTGCCAGACACACAGAGCAAAATGTGTAGCAAGCATCATGCCCTACCTTGCTGAGAG	2115
OY	901	GTGACAGTTTCTCATGTAGAGACGTGCAGAAAGAAATTAATAGCCAGCCAACTTAACCCA	960
Db	2116	GTGACAGTTTCTCATGTAGAGACGTGCAGAAAGAAATTAATAGCCAGCCAACTTAACCCA	2175
OY	961	GTGCTGAAAAGAAAAGAAATTAACCACTTTTGAAGAAATGTGCGCAGCATCCTTAACAA	1020
Db	2176	GTGCTGAAAAGAAAAGAAATTAACCACTTTTGAAGAAATGTGCGCAGCATCCTTAACAA	2235
OY	1021	GGCACACTCCCTAGCGCCCCCTGTGTGCTCATGTGTCGCGAGGAGGCCCAAGCCGAGT	1080
Db	2236	GGCACACTCCCTAGCGCCCCCTGTGTGCTCATGTGTCGCGAGGAGGCCCAAGCCGAGT	2295
OY	1081	CTTCCAAAGCCTCTCTCATCACTGATCAACAGCGCTGACGTGGCTGTGCTGCCGTGCCGT	1140
Db	2296	CTTCCAAAGCCTCTCTCATCACTGATCAACAGCGCTGACGTGGCTGTGCTGCCGTGCCGT	2355
OY	1141	AATGTGCTGTGTGATCTTGAAGCTGAGACATCTTGTGCTCAAGGCTCCAGAAAGAAATGG	1200
Db	2356	AATGTGCTGTGTGATCTTGAAGCTGAGACATCTTGTGCTCAAGGCTCCAGAAAGAAATGG	2415
OY	1201	AGAGGAGAAACTAGCTTAACGAGAAATGTGAGAGGGGACAGGTTTCTCCAGAGGAAAGGG	1260
Db	2416	AGAGGAGAAACTAGCTTAACGAGAAATGTGAGAGGGGACAGGTTTCTCCAGAGGAAAGGG	2475
OY	1261	GCTTCACAGTTCAGAGAAATTCACGAGAGTGTGGGACCTGCAGGAGATGTGGGACGCTGGGCG	1320

Db 2476 GCTCTCAAGTCCAGAGAAATTCAGAGAGTGGGAGCTGACAGAGTGGGACGCTGGGGC 2535
 Oy 1321 TGAGCGGGTGTGAAAGGCGAGAAAGGTGAAAAAGGCAAGCTGAAAGTCCCAATGTTTC 1380
 Db 2536 TGACCGGGTGTGAAAGGCGAGAAAGGTGAAAAAGGCGCAAGCTGAAAGTCCCAATGTTTC 2595
 Oy 1381 AGTGTGTTCACGGGGGCTGGGAGTTTCCGTGTCTCCGTGAGGCTTTATATCTTTCT 1440
 Db 2596 AGTGTGTTCACGGGGGCTGGGAGTTTCCGTGTCTCCGTGAGGCTTTATATCTTTCT 2655
 Oy 1441 CTGCTTGGAGAGAGAAAGTCTATTTCATGAAGGATGCAAGTTCATTAAGTCAAGCTGT 1500
 Db 2656 CTGCTTGGAGAGAGAAAGTCTATTTCATGAAGGATGCAAGTTCATTAAGTCAAGCTGT 2715
 Oy 1501 AAAATTCAGAGGTGTGCAATGGGTTTCTTTCACGAAGGCTTTATTTAATGGAATATAG 1560
 Db 2716 AAAATTCAGAGGTGTGCAATGGGTTTCTTTCACGAAGGCTTTATTTAATGGAATATAG 2775
 Oy 1561 GAAGGAGCTCATTTCTTAGGCGGTTAATTCACGGAGAAAGTGAAGTGAAGTCTTTCTT 1620
 Db 2776 GAAGGAGCTCATTTCTTAGGCGGTTAATTCACGGAGAAAGTGAAGTGAAGTCTTTCTT 2835
 Oy 1621 CATGTCTTCTGGGCAACTACTACAGCCCTGTGTGACTTGTGCTTAATGCAAGACGATCGAA 1680
 Db 2836 CATGTCTTCTGGGCAACTACTACAGCCCTGTGTGACTTGTGCTTAATGCAAGACGATCGAA 2895
 Oy 1681 AACTTGAATCAGAGAACTCGGTTTTCTTTCTGTGTTCTCCATTTGGTGTGCTGAC 1740
 Db 2896 AACTTGAATCAGAGAACTCGGTTTTCTTTCTGTGTTCTCCATTTGGTGTGCTGAC 2955
 Oy 1741 CGTGGGCAAGTGTCTCTCTCCGCGGCAATAGCTTCTGTGCTAATAAGACCTTGCA 1800
 Db 2956 CGTGGGCAAGTGTCTCTCTCCGCGGCAATAGCTTCTGTGCTAATAAGACCTTGCA 3015
 Oy 1801 GCTCTCGTGTCTGTGAACACTTCCCTGTGATTTCTGTGAGGGGGATGTTGAGAGGGG 1860
 Db 3016 GCTCTCGTGTCTGTGAACACTTCCCTGTGATTTCTGTGAGGGGGATGTTGAGAGGGG 3075
 Oy 1861 AAGAGGCGAGAGCTGGAGAGCTGAGCCACAGGGGAGGTGAGGGGGACAGAGAGCGAG 1920
 Db 3076 AAGAGGCGAGAGCTGGAGAGCTGAGCCACAGGGGAGGTGAGGGGGACAGAGAGCGAG 3135
 Oy 1921 CAGAGAGTGGGTCTCCATCAGTCCCATGATCACTGATCACTCAGAGACCGAGAGCCA 1980
 Db 3136 CAGAGAGTGGGTCTCCATCAGTCCCATGATCACTGATCACTCAGAGACCGAGAGCCA 3195
 Oy 1981 CAATGCTTCAGAGAAAGCTCAATGAACCCAAAGCCCAATTTTCTTCCCTTAAGCATAGAC 2040
 Db 3196 CAATGCTTCAGAGAAAGCTCAATGAACCCAAAGCCCAATTTTCTTCCCTTAAGCATAGAC 3255
 Oy 2041 AATGCAATTTGCCAATATACAAAAAGATGCAAGACTAATCTGTGTAGCTTTTGGCTG 2100
 Db 3256 AATGCAATTTGCCAATATACAAAAAGATGCAAGACTAATCTGTGTAGCTTTTGGCTG 3315
 Oy 2101 GCAATCAAAAACTGGGCGCAGAGCAAGTGAATAATGCAAGATGTTAATCTTTACGCC 2160
 Db 3316 GCAATCAAAAACTGGGCGCAGAGCAAGTGAATAATGCAAGATGTTAATCTTTACGCC 3375
 Oy 2161 TGAACGACACCCACGCACTCAGAGTACTGCTGACAGCAAGAGTACCTGCAAGCC 2220
 Db 3376 TGAACGACACCCACGCACTCAGAGTACTGCTGACAGCAAGAGTACCTGCAAGCC 3435
 Oy 2221 AGGGAGAGAGAGAGAGAGAGAGTGTATGACAGAGAAAGACAGATTCATTCAAG 2280
 Db 3436 AGGGAGAGAGAGAGAGAGAGAGTGTATGACAGAGAAAGACAGATTCATTCAAG 3495
 Oy 2281 GGAAGTGGGAATTTGACACAGAGATTTAGTCCACGTGATCCGTGGTTCTAGAGAGCAAG 2340
 Db 3496 GGAAGTGGGAATTTGACACAGAGATTTAGTCCACGTGATCCGTGGTTCTAGAGAGCAAG 3555
 Oy 2341 GCTATATTGTGGGGAGAAAAATCAATTCAAGGAAGTGGGAGACCTGATTTCTAATAC 2400

Db 3556 GCTATATTGTGGGGAGAAAAATCAAGTTCAGAGGAAGTCCGAGACCTGATTTCTAATAC 3615
 Oy 2401 TATATTTTCTTTTACAAAGCTGAGTAATTCAGAGCAAGTCAAGAGTATGAGGCT 2460
 Db 3616 TATATTTTCTTTTACAAAGCTGAGTAATTCAGAGCAAGTCAAGAGTATGAGGCT 3675
 Oy 2461 GTAAGATTACTTATAGTTTCTCCCTAATTAGAACTCTTTTCTCTGTGAGTTAGCAGACA 2520
 Db 3676 GTAAGATTACTTATAGTTTCTCCCTAATTAGAACTCTTTTCTCTGTGAGTTAGCAGACA 3735
 Oy 2521 AGGGCAATCCCGTTTCTTTTACAGAGAGAAACAATCCTAAGGTAAAGCAAGAT 2580
 Db 3736 AGGGCAATCCCGTTTCTTTTACAGAGAGAAACAATCCTAAGGTAAAGCAAGAT 3795
 Oy 2581 TCAAGCCTAGGCTTGTGCTGACTATATGATTTGTTTTGAAAAATCATTTCAAGGATGT 2640
 Db 3796 TCAAGCCTAGGCTTGTGCTGACTATATGATTTGTTTTGAAAAATCATTTCAAGGATGT 3855
 Oy 2641 TACTATCTGATTCAGAAAAATGAGACTAGTACCCTTTGGTCACTGTAAACAAACCCAT 2700
 Db 3856 TACTATCTGATTCAGAAAAATGAGACTAGTACCCTTTGGTCACTGTAAACAAACCCAT 3915
 Oy 2701 TTGTAAATGTCTCAAGTTCAAGGCTTAATCTGAGAAACCAATCAATTAAGATAGAACTTT 2760
 Db 3916 TTGTAAATGTCTCAAGTTCAAGGCTTAATCTGAGAAACCAATCAATTAAGATAGAACTTT 3975
 Oy 2761 AGAGCAAACTGTGTTTCTCCACTCTGAGAGTGAAGTCCAGGCAAGTTTGAATAATTT 2820
 Db 3976 AGAGCAAACTGTGTTTCTCCACTCTGAGAGTGAAGTCCAGGCAAGTTTGAATAATTT 4035
 Oy 2821 ACTTCACAAAGTATGACACTGTGTGTGATTAACAATTAAGTGTCTCAAGGCAATC 2880
 Db 4036 ACTTCACAAAGTATGACACTGTGTGTGATTAACAATTAAGTGTCTCAAGGCAATC 4095
 Oy 2881 ATATTTCAAGTGTCTTAAAGTACTCTGACAGTGTGTGATTAATTTATGCTATATGCC 2940
 Db 4096 ATATTTCAAGTGTCTTAAAGTACTCTGACAGTGTGTGATTAATTTATGCTATATGCC 4155
 Oy 2941 AATTTGCTTTTGTGTTTTCTCTTGGGTTTATATGTAAGACAGGATTTAATCACTAC 3000
 Db 4156 AATTTGCTTTTGTGTTTTCTCTTGGGTTTATATGTAAGACAGGATTTAATCACTAC 4215
 Oy 3001 AGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATTAATTTTGTGTTTACACCTT 3060
 Db 4216 AGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATTAATTTTGTGTTTACACCTT 4275
 Oy 3061 CTAATTAATTTAATTTATTTATTCATGCGAATTAAGACCTAATCTAAGTGTATA 3120
 Db 4276 CTAATTAATTTAATTTATTTATTCATGCGAATTAAGACCTAATCTAAGTGTATA 4335
 Oy 3121 ACAGTACCTGATTTGTCAATTAACATTAAGAAATCAGACATTTTACTATATTACA 3180
 Db 4336 ACAGTACCTGATTTGTCAATTAACATTAAGAAATCAGACATTTTACTATATTACA 4395
 Oy 3181 GTTGTGAGATACCTGTGAATTAATTAATTAATCTCAAAACATACTTGAATTAAGAC 3240
 Db 4396 GTTGTGAGATACCTGTGAATTAATTAATTAATTAATCTCAAAACATACTTGAATTAAGAC 4455
 Oy 3241 TCTCTGTGATCTGTTTTTAACATTTAATTAACATGTTTAAATTTGATATTTGA 3300
 Db 4456 TCTCTGTGATCTGTTTTTAACATTTAATTAACATGTTTAAATTTGATATTTGA 4515
 Oy 3301 TAAATATTTTCAATATCAATTTGTTCCCTTGTATATATATTTATTTAATTTGAACA 3360
 Db 4516 TAAATATTTTCAATATCAATTTGTTCCCTTGTATATATATTTATTTAATTTGAACA 4575
 Oy 3361 TCTTTCTGAGAGATTTCCCAAGATTTTCAACATGAGGTTCTTGGACATGACACACAG 3420
 Db 4576 TCTTTCTGAGAGATTTCCCAAGATTTTCAACATGAGGTTCTTGGACATGACACACAG 4635
 Oy 3421 AGTAAAGACTGATTTAGAGGCTTAACATTTGACATTTGGTGTCTGAGATGCAAGCTGAAT 3480
 Db 4636 AGTAAAGACTGATTTAGAGGCTTAACATTTGACATTTGGTGTCTGAGATGCAAGCTGAAT 4695

Query Match 67.6%; Score 4057.4; DB 3; Length 5304;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4077; Conservative 0; Mismatches 6; Indels 6; Gaps 1;

1 GCTCCACAGGAAGTCTCCCACTTAGACTTCGATCAGCATGTAAACGACGAGAAGCTC 60

Db	1216	GCTCACAAGGAAGTCTCCCACTCTAGACTTCTGCATACCAATGTATACGCCAAGAGCTC	1275
QY	61	CGTAGGGGTGAAGGCTCTGTGTCTTAACACTGATATGCTCTACACTGAGCTCACTGC	120
Db	1276	CGTAGGGGTGAAGGCTCTGTGTCTTAACACTGATATGCTCTACACTGAGCTCACTGC	1335
QY	121	AACCTGACCTCCCAAGGTTCAGAAATTCCTCTGTCTCAAGCTCCCGGTAGCTGGAGCT	180
Db	1336	AACCTGACCTCCCAAGGTTCAGAAATTCCTCTGTCTCAAGCTCCCGGTAGCTGGAGCT	1395
QY	181	AACGCGCAGCCCGGCTAAATTTTGTATGTGTAGAGATGGGGTTTCAACAATATAG	240
Db	1396	AACGCGCAGCCCGGCTAAATTTTGTATGTGTAGAGATGGGGTTTCAACAATATAG	1455
QY	241	CCCGGCTGTGTCTTGAACCTCCTGACCTCAGGTATCAACCCACTCAGCCTCTTAAAGTGC	300
Db	1456	CCCGGCTGTGTCTTGAACCTCCTGACCTCAGGTATCAACCCACTCAGCCTCTTAAAGTGC	1515
QY	301	TGGGATTTACAGGATAGATCAACCGCGCCCGGCGCAAGGGTCAGTGTTTATATAGAAATAC	360
Db	1516	TGGGATTTACAGGATAGATCAACCGCGCCCGGCGCAAGGGTCAGTGTTTATATAGAAATAC	1575
QY	361	TTGATGGTTTACTTAACCAACAGGGAAACGAAACAAAGCTGTATATTTTCAAGGATTC	420
Db	1576	TTGATGGTTTACTTAACCAACAGGGAAACGAAACAAAGCTGTATATTTTCAAGGATTC	1635
QY	421	TTGGGATGGGGAATGTGTCCATGTAGCTGCCTGACTAGTCCAGACCACTGGTCTCTATCA	480
Db	1636	TTGGGATGGGGAATGTGTCCATGTAGCTGCCTGACTAGTCCAGACCACTGGTCTCTATCA	1695
QY	481	CTTTCTTCCTCATCTCATATTTTCAGGCTAAGTACATTTATTTATCAACATGCTTTTGTG	540
Db	1696	CTTTCTTCCTCATCTCATATTTTCAGGCTAAGTACATTTATTTATCAACATGCTTTTGTG	1755
QY	541	GTAAGCCTCCACATGCTTACTGAAATTAAGATATATCAATACTAGTTCATTTGGGCGCA	600
Db	1756	GTAAGCCTCCACATGCTTACTGAAATTAAGATATATCAATACTAGTTCATTTGGGCGCA	1815
QY	601	TCTGTGTGTGTGTATTAAGGGAGAGAGGACATACCCCAAGACCTCCTTGAAGCCCCGGGAG	660
Db	1816	TCTGTGTGTGTGTATTAAGGGAGAGAGGACATACCCCAAGACCTCCTTGAAGCCCCGGGAG	1875
QY	661	AGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAGACCCCGGGGTCTGGGTCTCTGAGCA	720
Db	1876	AGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAGACCCCGGGGTCTGGGTCTCTGAGCA	1935
QY	721	ACCTGCCAGCCCGGTGCACATGTGTGTGTGTATCACTCTCTAGGAGCTGTGTCTTCT	780
Db	1936	ACCTGCCAGCCCGGTGCACATGTGTGTGTGTATCACTCTCTAGGAGCTGTGTCTTCT	1995
QY	781	ATTTCTGTGTGATCGTTCATTTATATCAAGGACATTCATGACAAATTTATATAGACTTATA	840
Db	1996	ATTTCTGTGTGATCGTTCATTTATATCAAGGACATTCATGACAAATTTATATAGACTTATA	2055
QY	841	TCTGCACAGACCAAGACAAATATGTGACAAAGACGTCACTGCCCTTACCTTCTGTGAG	900
Db	2056	TCTGCACAGACCAAGACAAATATGTGACAAAGACGTCACTGCCCTTACCTTCTGTGAG	2115
QY	901	GTGACAGTTTCTCATGTGAAGCGTGACAGAAATAATATAGCCAGCACTTAAACCA	960
Db	2116	GTGACAGTTTCTCATGTGAAGCGTGACAGAAATAATATAGCCAGCACTTAAACCA	2175
QY	961	GTGTGTAAATAAAGAAATTAACAACATCTTGAAGAAATGTGTGGCAGCATCCTTAAACAA	1020
Db	2176	GTGTGTAAATAAAGAAATTAACAACATCTTGAAGAAATGTGTGGCAGCATCCTTAAACAA	2235
QY	1021	GGCACCCTCCCTAGAGCGCCCTGTCTGCTCATCTGTGCGCGAGAGGCCCAACCCGAGT	1080
Db	2236	GGCACCCTCCCTAGAGCGCCCTGTCTGCTCATCTGTGCGCGAGAGGCCCAACCCGAGT	2295
QY	1081	CTTTCAGAGCTCTCTCTCATCATGTCACAGCGCTGACGTGCTGCTTCCCTGTG	1140

Db 2296 CTTCCAAAGCTCTCTCTCCATCAAGTCACAGGCGCTGACAGCTGCGCTTCCCTTCCCTG 2355
 Qy 1141 AATGCTCTGATGATCTGAGCTGAGACTCTCTTGAGCTCCAGGCTCCAGAAAGGAATG 1200
 Db 2256 AATGCTCTGATGATCTGAGCTGAGACTCTCTTGAGCTCCAGGCTCCAGAAAGGAATG 2415
 Qy 1201 AGAGGAAACTAGTCTAAGGAAATCTGAGGAGCAGTGTCTTCTCAGAGGGAAGG 1260
 Db 2416 AGAGGAAACTAGTCTAAGGAAATCTGAGGAGCAGTGTCTTCTCAGAGGGAAGG 2475
 Qy 1261 GCTTCCAGTCCAGGAAATTCAGAGGAGTGGGACTGCAAGAGAGTGGGAGCGTGGGC 1320
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 Qy 1741 CGTGGCAAGTGTCTCTCTCCCTGAGCCATAGTCTTCTGCTAATAAAGCCCTTGA 1800
 Db 2956 CGTGGCAAGTGTCTCTCTCCCTGAGCCATAGTCTTCTGCTAATAAAGCCCTTGA 3015
 Qy 1801 GCTCTGTGTCTGTGAACAATTCCCTGTGATTTCTGTGAGGAGGAGATGTTGAAGGAG 1860
 Db 3016 GCTCTGTGTCTGTGAACAATTCCCTGTGATTTCTGTGAGGAGGAGATGTTGAAGGAG 3075
 Qy 1861 AAGGAGGAGAGTGAAGAGTGAAGCCACAGGAGAGTGGAGAGGAGAGAGAGG 1920
 Db 3076 AAGGAGGAGAGTGAAGAGTGAAGCCACAGGAGAGTGGAGAGGAGAGAGAGG 3135
 Qy 1921 CAGAAAGTGGTGTCTCATCACTGCTCATCTGATCACTGATCACTCCAGAGCCGAGAGCCA 1980
 Db 3136 CAGAAAGTGGTGTCTCATCACTGCTCATCTGATCACTGATCACTCCAGAGCCGAGAGCCA 3195
 Qy 1981 CAATGCTTCAAGAAAGCTCAATGAACCCACAGCCCAATTTTCTTCCCTAAGCATAGAC 2040
 Db 3196 CAATGCTTCAAGAAAGCTCAATGAACCCACAGCCCAATTTTCTTCCCTAAGCATAGAC 3255
 Qy 2041 AATGGAATTTGCCAATAATACAAAGAAATGACAGAGCTAACTGAGTGGTGGCTTTGCCG 2100
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 Qy 2101 GCATTCAAAACTGGGCGAGAGCAATGAAAAATGACAGAGATGTTAACTTTTACCC 2160
 Db 3316 GCATTCAAAACTGGGCGAGAGCAATGAAAAATGACAGAGATGTTAACTTTTACCC 3375
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 Db 3376 TGAACGAGACCCACGAGCTCAGAGTGACTGCTGAACAGACGAGAGTGACTGCAAGCC 3435

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 Qy 2641 TACTATCTGATTCAGAAATAGAGCTAGTACCCCTTGTGCTGCTGTAACAAACACCAT 2700
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 Db 4396 GTTGTGAGATAGTGTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4455
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[illegible]

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Oy 961 GTGCTGAAGAAAGAAATTAACACCATCTTGAAAGATTTGCGCAGCATCCCTTAACA 1020
 Db 2176 GTGCTGAAGAAAGAAATTAACACCATCTTGAAAGATTTGCGCAGCATCCCTTAACA 2235
 Oy 1021 GGCCACCTTCCCTAGCGCCCTGCTGCTCCATCGTCGCCCGAGAGCCCCCAAGCCGAGT 1080
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 Oy 1081 CTTCCAAACCTCCTCCTCATCAGTCACAGCGCTGCACCTGGCCCTCCGCTTCCCGTG 1140
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 Oy 1141 AATCGTCTGCTGATCTGAGCTGAGAGACTCTTGAGCTCAAGCTCCAGAAAAGAAATAG 1200
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 Db 2536 TGAAGCGGCTGTGAAGGAGAGAGGTGAAAAGGCAAGGCTGAAGCTGCCAGATGTTTC 2595
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 Oy 1861 AAGAGAGCAGAGCTGAGAGAGCTGAGAGCAGGAGGAGTGAAGGGGAGCAGGAAGCAG 1920
 Db 3076 AAGAGAGCAGAGCTGAGAGAGCTGAGAGCAGGAGGAGTGAAGGGGAGCAGGAAGCAG 3135
 Oy 1921 CAGAAAGCTGGTGTCTCATCAAGTCTCATCTGATCACTGACAGCTCCAGAGCCGAGGCCA 1980
 Db 3136 CAGAAAGCTGGTGTCTCATCAAGTCTCATCTGATCACTGACAGCTCCAGAGCCGAGGCCA 3195
 Oy 1981 CATGTCTTCAAGAAAGCTCAATGAACCCAGCCAGCATTTTCTTCTTCCCTAAGCATAGAC 2040
 Db 3196 CATGTCTTCAAGAAAGCTCAATGAACCCAGCCAGCATTTTCTTCTTCCCTAAGCATAGAC 3255

Oy 2041 AATGCAATTTGCCAATTAACCAAAAAGATGAGAGACTAACTGTGTGTAGCTTTTGCTG 2100
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 Oy 2221 AGGGAGAGAGAAAGAAAAGAGAGGAGATAGTATAGCAAGAAAGACAGATTCATTCAAG 2280
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 Oy 2880 CATTAATTTCAAGTGCCTAAAGTTACTCTGACAGTTTGGATTAATTAATGCTAATAGC 2939
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 Oy 2940 CATTTGCTTTTGTGTTTTTCTCTTGGGTTTATTAATGAAGGAGGATTAATTAACCTA 2999
 Db 4155 CATTTGCTTTTGTGTTTTTCTCTTGGGTTTATTAATGAAGGAGGATTAATTAACCTA 4214
 Oy 3000 CAGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATTAATTTTGTGTTTACACCT 3059
 Db 4215 CAGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATTAATTTTGTGTTTACACCT 4274
 Oy 3060 TCTAATTAATTTTAATTTTATTTTCCATTTGGAATAGAGCCATAACTCAAGTGGTAT 3119
 Db 4275 TCTAATTAATTTTAATTTTATTTTCCATTTGGAATAGAGCCATAACTCAAGTGGTAT 4334
 Oy 3120 AACAGTACCTGTGATTTGTCAATTAACCAATAGAAATCAAGACATTTTATCTAATATAC 3179


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Db      4335 AACAGTACCTGTAATTTTGCATTAACCAATAGAAATCAGACATTTTATATATATAC 4394
Qy      3180 AGTTGTGCAGATACGTTGTAGTGAATATTTATCTCAAACTACTTTGAAATAGAC 3239
Db      4395 AGTTGTGCAGATACGTTGTAGTGAATATTTATCTCAAACTACTTTGAAATAGAC 4454
Qy      3240 CTCCTGCTGAGCTTGTGTTTAAATATTAATTAATTAATTAATTAATTAATTTG 3299
Db      4455 CTCCTGCTGAGCTTGTGTTTAAATATTAATTAATTAATTAATTTGATTTTG 4514
Qy      3300 ATATCATATTTTCAATATATCTTTGTTTCTTTGTAATCTATATTTTATATTTGAAAC 3359
Db      4515 ATATCATATTTTCAATATATCTTTGTTTCTTTGTAATCTATATTTTATATTTGAAAC 4574
Qy      3360 ATCTTTCTGAGAGAGTCCCGAGATTTCCAGATAGAGGTTCTTGAGATGACACACACA 3419
Db      4575 ATCTTTCTGAGAGAGTCCCGAGATTTCCAGATAGAGGTTCTTGAGATGACACACACA 4634
Qy      3420 GAGTAAAGAACTGATTTAGAGGCTAATGACATTTGAGTGGCTGAGATGCAAGACTGAAT 3479
Db      4635 GAGTAAAGAACTGATTTAGAGGCTAATGACATTTGAGTGGCTGAGATGCAAGACTGAAT 4694
Qy      3480 TAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTAGAGGGGAAATCTG 3539
Db      4695 TAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTAGAGGGGAAATCTG 4754
Qy      3540 CCGCTCTTAGAGAAAGTCTCCCTGAGAGCTGTTAGGGGTGCTGTCTGTCTGTCTGCT 3599
Db      4755 CCGCTCTTAGAGAAAGTCTCCCTGAGAGCTGTTAGGGGTGCTGTCTGTCTGTCTGCT 4814
Qy      3600 GCGTGTATTTTCTCTGCTCCCTGCTAGCTCTTAAGAGACTTGTGTAATCTCAGTTCC 3659
Db      4815 GCGTGTATTTTCTCTGCTCCCTGCTAGCTCTTAAGAGACTTGTGTAATCTCAGTTCC 4874
Qy      3660 TAGCATAGTGCCTGSCACAGTGCAGGTTCTCAATGAGTTGCAAGATGAAATATA 3719
Db      4875 TAGCATAGTGCCTGSCACAGTGCAGGTTCTCAATGAGTTGCAAGATGAAATATA 4934
Qy      3720 AACTAGAAATATATCTTGTGTAATCAGACACACAGTACTGCTGTGTAAGTGTGTA 3779
Db      4935 AACTAGAAATATATCTTGTGTAATCAGACACACAGTACTGCTGTGTAAGTGTGTA 4994
Qy      3780 C--GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3837
Db      4995 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5054
Qy      3838 GGGGTATGGGTGATTAATTTGGAGTCTTTTAAAGAACTCCAAACAGACTTCTG 3897
Db      5055 GGGGTATGGGTGATTAATTTGGAGTCTTTTAAAGAACTCCAAACAGACTTCTG 5114
Qy      3898 GAAAGTATTTTCTAAGATCTTGTGAGAGGTGAAGGCAACCCCTGTGTGACAGCCC 3957
Db      5115 GAAAGTATTTTCTAAGATCTTGTGAGAGGTGAAGGCAACCCCTGTGTGACAGCCC 5174
Qy      3958 CACCAAGCCTCAGTGGCAGCTGTCTTCCCAATGAAGGAGTGGCTCCCAAGATAT 4017
Db      5175 CACCAAGCCTCAGTGGCAGCTGTCTTCCCAATGAAGGAGTGGCTCCCAAGATAT 5234
Qy      4018 ATAAACCTCTGAGAGCTCAGGATGAGGCAAGCAAG 4054
Db      5235 ATAAACCTCTGAGAGCTCAGGATGAGGCAAGCAAG 5271

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RESULT 8

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US-09-056-285A-1
; Sequence 1, Application US/09056285A
; Patent No. 6403307
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; Sheffield, Val C.
; Alward, Wallace L.M.
; Fingert, John

```

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; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,285A
; FILING DATE: 07-Apr-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-010.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-056-285A-1

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Query Match      46.2%; Score 2773.4; DB 3; Length 2800;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2797; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

Qy      2216 AGCGAGGGGAGGAGAAAGAAAGAGAGGATGATGATGATGATGATGATGATGATGAT 2275
Db      1 AGCGAGGGGAGGAGAAAG-AAAAGAGGGGATGATGATGATGATGATGATGATGATGAT 59

Qy      2276 TCAAGGGGAGTGGGAAATGACACAGAGGATTAATATCCACCGATCTGGGTTCTAGAG 2335
Db      60 TCAAGGGGAGTGGGAAATGACACAGAGGATTAATATCCACCGATCTGGGTTCTAGAG 119

Qy      2336 GCAGGGCTATATTTGTGGGGGAAAGAAATCAGTTCAAGGAAAGTCCGGAGACTGATTTCT 2395
Db      120 GCAGGGCTATATTTGTGGGGGAAAGAAATCAGTTCAAGGAAAGTCCGGAGACTGATTTCT 179

Qy      2396 AATATCTATATTTTCTTTTACAGCTGATTAATCTGAGCAAGTCAAGAGTAGTAATCTG 2455
Db      180 AATATCTATATTTTCTTTTACAGCTGATTAATCTGAGCAAGTCAAGAGTAGTAATCTG 239

Qy      2456 AGGCTGTAAAGATTAATTTAGTTTCTCCTTATTAAGAACTTTTCTCTGTGAGTTACCA 2515
Db      240 AGGCTGTAAAGATTAATTTAGTTTCTCCTTATTAAGAACTTTTCTCTGTGAGTTACCA 299

Qy      2516 GCACAAGGCAATCCCGTTTCTTTTACAGGAAGAAACATTTCTTAAGATTAAGCCAAA 2575
Db      300 GCACAAGGCAATCCCGTTTCTTTTACAGGAAGAAACATTTCTTAAGATTAAGCCAAA 359

Qy      2576 CAGATTCAAGCTTAGTGTGCTGACATATATGATTTGTTTTTGAATAATCATTTACGCG 2635
Db      360 CAGATTCAAGCTTAGTGTGCTGACATATATGATTTGTTTTTGAATAATCATTTACGCG 419

Qy      2636 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCTTTGTGAGCTGTAACAAACA 2695
Db      420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCTTTGTGAGCTGTAACAAACA 479

Qy      2696 CCCATTGTATATGCTCAAGTTCAAGGCTTAAGTCAAGAACCAATCAATTAAGATAGAA 2755
Db      480 CCCATTGTATATGCTCAAGTTCAAGGCTTAAGTCAAGAACCAATCAATTAAGATAGAA 539

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[illegible]

Qy	3834	TATTGGGATATGGGTGCATTAATTGGGATGTCTTTTAAAAAGAACTCCCAACAGACT	3893
Db	1620	TATTGGGATATGGGTGCATTAATTGGGATGTCTTTTAAAAAGAACTCCCAACAGACT	1679
Qy	3894	TCGGAAGGTTATTTCTTAAGATCTTGCTGGCAGCTGAAGGCAACCCCTGTGCACA	3953
Db	1660	TCGGAAGGTTATTTCTTAAGATCTTGCTGGCAGCTGAAGGCAACCCCTGTGCACA	1739
Qy	3954	GGCCCAACGAGCTCAGCTGGGCCAAGCTGTCTGTCTTCCCATGAAGGCTGGCTCCCAAT	4013
Db	1740	GGCCCAACGAGCTCAGCTGGGCCAAGCTGTCTGTCTTCCCATGAAGGCTGGCTCCCAAT	1799
Qy	4014	ATATATTAACCTCTCTCGAGCTCAGGCAATGACCCAGCAAGGCCAACCACACAGGCACTC	4073
Db	1800	ATATATTAACCTCTCTCGAGCTCAGGCAATGACCCAGCAAGGCCAACCACACAGGCACTC	1859
Qy	4074	TCAGACACGACAGGCTTTCAGAGGAAGCCTCACCAAGCCTCTGCATATGAGTTCTTCTG	4133
Db	1860	TCAGACACGACAGGCTTTCAGAGGAAGCCTCACCAAGCCTCTGCATATGAGTTCTTCTG	1919
Qy	4134	TCACAGTTGCTCAGCTTGTGGCCTGAGATGCCAGCTGTCCAGTCTGCTGTCTTGACCTG	4193
Db	1920	TCACAGTTGCTCAGCTTGTGGCCTGAGATGCCAGCTGTCCAGTCTGCTGTCTTGACCTG	1979
Qy	4194	CCTGTGTGGGATGTGTGGGGCCACAGACACTGACTCAGAAAGGCCAATGACAGAGTGG	4253
Db	1980	CCTGTGTGGGATGTGTGGGGCCACAGACACTGACTCAGAAAGGCCAATGACAGAGTGG	2039
Qy	4254	CCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAAATCCAGCTGCCACAGACAG	4313
Db	2040	CCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAAATCCAGCTGCCACAGACAG	2099
Qy	4314	CCAGGCAATGTCAAGTCATCCATTAATTACAGAGACACAGACACCCAAAGCTTAGACT	4373
Db	2100	CCAGGCAATGTCAAGTCATCCATTAATTACAGAGACACAGACACCCAAAGCTTAGACT	2159
Qy	4374	GGAGGCCACAAAGCTGCACTCAGGCTCCCTGAGAGAGCTTCCTCAACCAATTGACCTTGA	4433
Db	2160	GGAGGCCACAAAGCTGCACTCAGGCTCCCTGAGAGAGCTTCCTCAACCAATTGACCTTGA	2219
Qy	4434	CCAGGCTGCCAGGCCCCCAAGGACCCACAGAGGGGGCTGCAGAGGGAGCTGGGGACCTTGAG	4493
Db	2220	CCAGGCTGCCAGGCCCCCAAGGACCCACAGAGGGGGCTGCAGAGGGAGCTGGGGACCTTGAG	2279
Qy	4494	GGGGAGCGGGACAGCTGGAAACCCAAACAGAGATTGGAAGCTGCTTACAGCAACT	4553
Db	2280	GGGGAGCGGGACAGCTGGAAACCCAAACAGAGATTGGAAGCTGCTTACAGCAACT	2339
Qy	4554	CCTCCAGACAGTCAAGTTCTGAGAGAAAGAAAGCACTAAGGCAAGAAATGAGAA	4613
Db	2340	CCTCCAGACAGTCAAGTTCTGAGAGAAAGAAAGCACTAAGGCAAGAAATGAGAA	2399
Qy	4614	TCGTGCCAGAGGTTGGAAAGCAGACCCAGAGGTAGCAAGGCTGAGAAAGGGGCGCAGTG	4673
Db	2400	TCGTGCCAGAGGTTGGAAAGCAGACCCAGAGGTAGCAAGGCTGAGAAAGGGGCGCAGTG	2459
Qy	4674	TCGCCAAGCCGAGACACTGCTCGGGCTGTGCCACAGGCTCCAGAGAAAGTAAAGATGC	4733
Db	2460	TCGCCAAGCCGAGACACTGCTCGGGCTGTGCCACAGGCTCCAGAGAAAGTAAAGATGC	2519
Qy	4734	AGAGTGGGGGAGCTCTGAAGTTCAGCAGGTGATATGGCTCTGTAAGTGAACCTGTACAGGGGC	4793
Db	2520	AGAGTGGGGGAGCTCTGAAGTTCAGCAGGTGATATGGCTCTGTAAGTGAACCTGTACAGGGGC	2579
Qy	4794	TCGAGGCTCCCTGCGCCCTTCTCTCTAGAGCTGACAGAGCTAGCACAAGACAGATGA	4853
Db	2580	TCGAGGCTCCCTGCGCCCTTCTCTCTAGAGCTGACAGAGCTAGCACAAGACAGATGA	2639
Qy	4854	ATTAAAGAAAGCAGAGCATCACTTCAAGTATTAAGTAATTTAGCTCTCGAGAGCTT	4913
Db	2640	ATTAAAGAAAGCAGAGCATCACTTCAAGTATTAAGTAATTTAGCTCTCGAGAGCTT	2699
Qy	4914	CATTYAGATTAGTGGTTCAGAGTCTTGTGGCCCTCCATGTCAGTTTTCACAGTCCATAG	4973

Db	Qy	Db
2760	4974	2760
CATTAGATTAGTGTTCAGAGTTCTTGTGCCCTCCATGTCAGATTTCACAGTCCATAG	CAAAAGAGAAATAAAGGACCCGGGTGAGATGTGTCTTCAT	CAAAAGAGAAATAAAGGACCCGGGTGAGATGTGTCTTCAT
2800	5014	2800
CAAAAGAGAAATAAAGGACCCGGGTGAGATGTGTCTTCAT	CAAAAGAGAAATAAAGGACCCGGGTGAGATGTGTCTTCAT	CAAAAGAGAAATAAAGGACCCGGGTGAGATGTGTCTTCAT

RESULT 9

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US-10-017-870-10
; Sequence 10, Application US/10017870
; Patent No. 6727354
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUII
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
; CURRENT APPLICATION NUMBER: US/10/017,870
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-870-10

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Query Match	46.2%	Score 2773.4	DB 3	Length 2800
Best Local Similarity	99.9%	Pred. No. 0		
Matches 2797; Conservative	0	Mismatches	1	Indels 3; Gaps 2

QY	2216	GGCCGAGGGGAGGAGAGAAAAAGAGGGGATAGTGATATGAGCAAGAAAGCAATTCAT	2275
Db	1	AGCCGAGGGGAGGAGAGAG-AAAAGAGGGGATAGTGATGAGCAAGAAAGCAATTCAT	59
QY	2276	TCAAGGCGAGTGGGAATTGACCAAGGATTTATAGTCCACGTGATCTCGGGTTTACAGAG	2335
Db	60	TCAAGGGGAGTGGGAATTGACCAAGGATTTATAGTCCAAGTATCTCGGGTTTACAGAG	119
QY	2336	GCAGGGCTATTTGTGGGGGGGAAAAATCAATTCAAGGAAGTGGGAGACTGATTTCT	2395
Db	120	GCAGGGCTATTTGTGGGGGGGAAAAATCAATTCAAGGAAGTGGGAGACTGATTTCT	179
QY	2396	AATACTATATTTTCTCTTAAAGCTGAGTAACTCTGAGCAAGTCACAGGTAGTAACTG	2455
Db	180	AATACTATATTTTCTCTTAAAGCTGAGTAACTCTGAGCAAGTCACAGGTAGTAACTG	239
QY	2456	AGGCTGTAGAATTACTTAGTTCTCTCTTATTAGGACCTCTTCTCTGTGAGTTAGCA	2515
Db	240	AGGCTGTAGAATTACTTAGTTCTCTCTTATTAGGACCTCTTCTCTGTGAGTTAGCA	259
QY	2516	GCACAGGGCAATCCCGTTTCTTTTAAACAGAGAAAACTTCTTAAGTAAAGCCAA	2575
Db	300	GCACAGGGCAATCCCGTTTCTTTTAAACAGAGAAAACTTCTTAAGTAAAGCCAA	359
QY	2576	CAGATTCAAGGCTAGTCTGTGCTGACATATATGATGTGTTTTGAAAAATCATTTACGC	2635
Db	360	CAGATTCAAGGCTAGTCTGTGCTGACATATATGATGTGTTTTGAAAAATCATTTACGC	419
QY	2636	ATGTTTACTATCTGATTCAGAAAAATGAGACTAGACCTTGTGCTCACTGTAAACAACA	2695
Db	420	ATGTTTACTATCTGATTCAGAAAAATGAGACTAGACCTTGTGCTCACTGTAAACAACA	479
QY	2696	CCCATTTGTAAATGTCACAGTTCAAGCTTAACTGCGAAGCCAAATCAAATTAAGATAGAA	2755
Db	480	CCCATTTGTAAATGTCACAGTTCAAGCTTAACTGCGAAGCCAAATCAAATTAAGATAGAA	539
QY	2756	TCATTAGAGCAACGTGTGTTCTCACACTGAGAGTAGTCTGCGACAGGAGTGTGGAAA	2815
Db	540	TCATTAGAGCAACGTGTGTTCTCACACTGAGAGTAGTCTGCGACAGGAGTGTGGAAA	599
QY	2816	TATTTACTTCAAGATATGCACTGTTGTGTGATTAAACAATAAAGTTGCTCAAAG	2875
Db	600	TATTTACTTCAAGATATGCACTGTTGTGTGATTAAACAATAAAGTTGCTCAAAG	659

[illegible]

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QY 3954 GCCCACCAGCTCAGGTGGCCACTCTGTTCTTCCCATGAAGGGCTGGCTCCCAAGT 4013
Db 1740 GCCCACCAGCTCAGGTGGCCACTCTGTTCTTCCCATGAAGGGCTGGCTCCCAAGT 1799
QY 4014 ATATATTAACCTCTCTGGAGCTCAGGCATGAGCCAGCAGGCCCAATCCAGGCACTC 4073
Db 1800 ATATATTAACCTCTCTGGAGCTCAGGCATGAGCCAGCAGGCCCAATCCAGGCACTC 1859
QY 4074 TCAGACACGAGAGCTTTCAGAGGAAGCTCACAAGACCTCTGCAATGAGTTCTTCTG 4133
Db 1860 TCAGACACGAGAGCTTTCAGAGGAAGCTCACAAGACCTCTGCAATGAGTTCTTCTG 1919
QY 4134 TGCAAGTTGCTGAGCTTTGGGCTTGAGATGCAAGCTGTCCAGCTGCTTCTGGCCCTG 4193
Db 1920 TGCAAGTTGCTGAGCTTTGGGCTTGAGATGCAAGCTGTCCAGCTGCTTCTGGCCCTG 1979
QY 4194 CTTGGTGTGGATGTGGGGGCAAGACAGCTCAGCTCAGGAAGGCCAATGACAGAGTGG 4253
Db 1980 CTTGGTGTGGATGTGGGGGCAAGACAGCTCAGCTCAGGAAGGCCAATGACAGAGTGG 2039
QY 4254 CCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTGCCAGAGAGAG 4313
Db 2040 CCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTGCCAGAGAGAG 2099
QY 4314 CCAAGCCATGTCAATCATCACTTAAGAGAGACAGCAGCACCAGCCTTAGACCT 4373
Db 2100 CCAAGCCATGTCAATCATCACTTAAGAGAGACAGCAGCACCAGCCTTAGACCT 2159
QY 4374 GAGAGCCCAAGAGCTCAGCTCAGCTCCCTGGAGAGCTCTCCACCAATGACCTTGGGA 4433
Db 2160 GAGAGCCCAAGAGCTCAGCTCAGCTCCCTGGAGAGCTCTCCACCAATGACCTTGGGA 2219
QY 4434 CCAAGCTGCCAGGCCCCAGAGAGACCCAGAGGGGCTGAGAGGGGAGCTGGGCAACCTGAG 4493
Db 2220 CCAAGCTGCCAGGCCCCAGAGAGACCCAGAGGGGCTGAGAGGGGAGCTGGGCAACCTGAG 2279
QY 4494 GCGGAGGCGGAGACAGCTGGAACCCAAACAGAGATTGAGACTGTCTACAGCAACT 4553
Db 2280 GCGGAGGCGGAGACAGCTGGAACCCAAACAGAGATTGAGACTGTCTACAGCAACT 2339
QY 4554 CCTCCGAGACAGAGTCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4613
Db 2340 CCTCCGAGACAGAGTCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2399
QY 4614 TCTGSCAGAGAGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4673
Db 2400 TCTGSCAGAGAGTTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2459
QY 4674 TCCCCAGACCCGAGACACTGCTCGGGCTGTGCAACAGGCTTCAGAGAGAGTAAAGATGC 4733
Db 2460 TCCCCAGACCCGAGACACTGCTCGGGCTGTGCAACAGGCTTCAGAGAGAGTAAAGATGC 2519
QY 4734 AGAGTGGGGGAGACTTGAAGTTCAAGAGAGTATGAGCTGTGATGACCTGCTACAGGGGC 4793
Db 2520 AGAGTGGGGGAGACTTGAAGTTCAAGAGAGTATGAGCTGTGATGACCTGCTACAGGGGC 2579
QY 4794 TCCAGGCTCCCTGCTGCTCCCTTCTCTCAGAGAGAGTGAACAGCTGACCAAGAGATGA 4853
Db 2580 TCCAGGCTCCCTGCTGCTCCCTTCTCTCAGAGAGAGTGAACAGCTGACCAAGAGATGA 2639
QY 4854 ATTAAGGAAGACAGAGCATCACTTCAAGTATTAAGTAAATTTAGTCTGAGAGCTT 4913
Db 2640 ATTAAGGAAGACAGAGCATCACTTCAAGTATTAAGTAAATTTAGTCTGAGAGCTT 2699
QY 4914 CATTTAGATTAGTGTTCAGAGTTCTTGTGCCCCCTCCATGTCAGATTTTCAAGTCCATAG 4973
Db 2700 CATTTAGATTAGTGTTCAGAGTTCTTGTGCCCCCTCCATGTCAGATTTTCAAGTCCATAG 2759
QY 4974 CAAAAGGAGAAATTAAGAGACCGGGTGAAGTGTCTGAT 5014
Db 2760 CAAAAGGAGAAATTAAGAGACCGGGTGAAGTGTCTGAT 2800

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RESULT 10
US-09-952-464A-1
; Sequence 1, Application US/09952464A
; Patient No. 6956103
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087.0017U1
; CURRENT APPLICATION NUMBER: US/09/952,464A
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 09/461,542
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence, No. 6956103e
; OTHER INFORMATION: Synthetic construct
US-09-952-464A-1

Query Match 46.2%; Score 2773.4; DB 3; Length 2800;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2797; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 2216 AGCCAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2275
Db 1 AGCCAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 59

QY 2276 TCAAGGCGAGTGGGAATTGACCAAGGATTAATGTCACGTGATCCTGGGTTCTAGAG 2335
Db 60 TCAAGGCGAGTGGGAATTGACCAAGGATTAATGTCACGTGATCCTGGGTTCTAGAG 119

QY 2336 GCAAGGCTATTTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2395
Db 120 GCAAGGCTATTTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179

QY 2396 AATCTATATTTTCTCTTCAAGCTGAGTAATCTGAGCAAGTCACAGGTAGTAAGT 2455
Db 180 AATCTATATTTTCTCTTCAAGCTGAGTAATCTGAGCAAGTCACAGGTAGTAAGT 239

QY 2456 AGGCTGAAGATTACTTATGTTCTCTTATTAGAACTCTTTTCTCTGTGAGTTAGCA 2515
Db 240 AGGCTGAAGATTACTTATGTTCTCTTATTAGAACTCTTTTCTCTGTGAGTTAGCA 299

QY 2516 GCAAGAGGCAATCCCGTTTCTTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2575
Db 300 GCAAGAGGCAATCCCGTTTCTTTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359

QY 2576 CAGATTCAAGGCTAGGCTCTGCTGACATATGATGTTGTTTGAAGAAATCATTTCAAG 2635
Db 360 CAGATTCAAGGCTAGGCTCTGCTGACATATGATGTTGTTTGAAGAAATCATTTCAAG 419

QY 2636 ATGTTTACTATCTGATTCAAGAAATGAGACTAGTACCCTTTGTGACGCTGTAACAAACA 2695
Db 420 ATGTTTACTATCTGATTCAAGAAATGAGACTAGTACCCTTTGTGACGCTGTAACAAACA 479

QY 2696 CCCATTGTAATATGCTCAAGTTCAAGGCTTAATCTGACAAACCAATCAATTAAGATAGAA 2755
Db 480 CCCATTGTAATATGCTCAAGTTCAAGGCTTAATCTGACAAACCAATCAATTAAGATAGAA 539

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QY 2756 TCTTTAGAGCAACTGTGTTTCTCCACTGAGGTGAGTCTGGCAGGGCAGTTGGAAA 2815
Db 540 TCTTTAGAGCAAAGTGTGTTTCTCCACTGAGGTGAGTCTGGCAGGGCAGTTGGAAA 599
QY 2816 TATTTACTTCAAGATATTTGACACTGTGTGGTATTAACAACATTAAGTTGCTCAAGG 2875
Db 600 TATTTACTTCAAGATATTTGACACTGTGTGGTATTAACAACATTAAGTTGCTCAAGG 659
QY 2876 CAATCATTTATTTAAGGAGCTTAAGTTACTCTGACAGTTGGTATTTATTTATGGCTA 2935
Db 660 CAATCATTTATTTAAGGAGCTTAAGTTACTCTGACAGTTGGTATTTATTTATGGCTA 719
QY 2936 TTGCAATTTGCTTTTGTGTTTCTCTTTGGGTTTATTAATGTAAGCAGGATTTATTA 2995
Db 720 TTGCAATTTGCTTTTGTGTTTCTCTTTGGGTTTATTAATGTAAGCAGGATTTATTA 779
QY 2996 CCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTAATTTTGTTTTACC 3055
Db 780 CCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTAATTTTGTTTTACC 839
QY 3056 ACCCTTAACATAATTTAATTTAATTTTATTCATTTGCCAATGAGCCATTAACCTCAAGTGG 3115
Db 840 ACCCTTAACATAATTTAATTTAATTTTATTCATTTGCCAATGAGCCATTAACCTCAAGTGG 899
QY 3116 TAAATAACAGTACCTGTGATTTGTCAATTAACAATGAAATCAAGACATTTTATCTATA 3175
Db 900 TAAATAACAGTACCTGTGATTTGTCAATTAACAATGAAATCAAGACATTTTATCTATA 959
QY 3176 TTACAGTTGTTGCAATACCTGTGAATGTAATATTTATTAATCTCAAAATCTAATTTGAAT 3235
Db 960 TTACAGTTGTTGCAATACCTGTGAATGTAATATTTATTAATCTCAAAATCTAATTTGAAT 1019
QY 3236 AGACCTCCGCGCTGAGTCTGTTTAAACATTAATTAACATGTTTAAATTTGATAT 3295
Db 1020 AGACCTCCGCGCTGAGTCTGTTTAAACATTAATTAACATGTTTAAATTTGATAT 1079
QY 3296 TTTGATATCATATTTCAATATCATTTGTTTCTTTGTAATCTATAATTTATTAATTTGA 3355
Db 1080 TTTGATATCATATTTCAATATCATTTGTTTCTTTGTAATCTATAATTTATTAATTTGA 1139
QY 3356 AAAACATCTTTCTGAGAAAGTCCCAAGATTTCAACATGAGGTTCTTGGCATGCACACA 3415
Db 1140 AAAACATCTTTCTGAGAAAGTCCCAAGATTTCAACATGAGGTTCTTGGCATGCACACA 1199
QY 3416 CACAGATTAAGAACTAATTTAGAGGCTAACATTTGAACATTTGCTCTGAATGCACACCTG 3475
Db 1200 CACAGATTAAGAACTAATTTAGAGGCTAACATTTGAACATTTGCTCTGAATGCACACCTG 1259
QY 3476 AAATTAAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAAGGGGTGAGGGGGGAAA 3535
Db 1260 AAATTAAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAAGGGGTGAGGGGGGAAA 1319
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Db 1320 TCTGCGGCTTTATAGAAATGCTCTCCCTGAGACCTGTAGAGGTGCTGTCTTGTGTTCT 1379
QY 3596 GGTGTGCTGTATTTTCTCTGTCTCTGTCTGCTAAGTCTTAAAGAACTTGTGTTGATCTTCAG 3655
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QY 3656 TTCTAGCATAGTACCTGAGCAAGTGCAGAGTTCTCAATAGATTGTCAGAGTGAATGGAAA 3715
Db 1440 TTCTAGCATAGTACCTGAGCAAGTGCAGAGTTCTCAATAGATTGTCAGAGTGAATGGAAA 1499
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QY 3834 TATTTGGGATATGAGGTGATTAATTTGGATGTTCTTTTAAAGAAATCTCAACAGACT 3893
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QY 3954 GCCCCACCCAGCTCACTGTGCTCACTGTCTTCTTCCCTCAATGAAGGCTGTGCCAGT 4013
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QY 4074 TCAGCAGCAGAGCTTTTCAAGAGAAAGCTCAACAAAGCTCTGCAATGAGTTCTTCTG 4133
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Db 2040 CCGATGCCAGTATACCTTCAAGTGTGGCCAGTCCCAATGAATCAGCTGCCAGAGACAGAG 2099
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QY 4494 GCGGGAGCGGGACCAAGCTGGAACCCCAACAGAGATTGAGACTGTCTTACAGCAACT 4553
Db 2280 GCGGGAGCGGGACCAAGCTGGAACCCCAACAGAGATTGAGACTGTCTTACAGCAACT 2339
QY 4554 CCTCCGAGCAAGTCAATTTCTGAGAGAGAGAAAGGACCTTAAGGCAAGAAATGAGAA 4613
Db 2340 CCTCCGAGCAAGTCAATTTCTGAGAGAGAGAAAGGACCTTAAGGCAAGAAATGAGAA 2399
QY 4614 TCTGCGCAGAGGTTGGAAGAGCAGCAGGAGGTTAGCAAGGCTGAGAGAGGGGCAAGT 4673
Db 2400 TCTGCGCAGAGGTTGGAAGAGCAGCAGGAGGTTAGCAAGGCTGAGAGAGGGGCAAGT 2459
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QY 4734 AGAGTGGGGGAGCTGTAGTTTCAAGAGGTGATATATGCTCTGTAGTACCTGTCAAGGGC 4793
Db 2520 AGAGTGGGGGAGCTGTAGTTTCAAGAGGTGATATGCTCTGTAGTACCTGTCAAGGGC 2579
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QY 4854 ATTTAAGAAAGCAGCAGCATCACTTCAAGTATTAATTAATTTAGTCTCTGAGAGCTT 4913
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Db 2700 CATTAGATTAGTGTGTCAGAGTTCTTGCCCTCCATGTCAGTTTTCAGAGTCCATAG 2759
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Db 2760 CAAAAGGAAATATAAGACCCGGTGAGTGTCTTCAT 2800

RESULT 11
US-08-822-999-1
; Sequence 1, Application US/08822999
; Patent No. 6271026
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; TITLE OF INVENTION: GLAUCOMA COMPOSITIONS AND THERAPEUTIC
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,999
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,347
; FILING DATE: 30-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/748,479
; FILING DATE: 08-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,218
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-010.27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-822-999-1

Query Match 12.8%; Score 770; DB 3; Length 2166;
Best local similarity 98.3%; Pred. No. 3.6e-178;
Matches 773; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 4000 GCTGGCTCCCGCATATATATAACCTCTCTGAGCTCAGGACGAGCGCAAGGCGACC 4059
Db 61 GCTGGCTCCCGCATATATATAACCTNTNTGAGNTGAGGACGAGCGCAAGGCGACC 120
Qy 4060 CATCCAGGACCTCTCAGCAGACAGAGCTTTCAGAGGAAGCCTCACCAGGCTCTGCA 4119

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Db 181 ATAGAGTTCTTCTGTGACAGCTGTGAGCTTTGGGCTGAGATGCCAGCTGCAGCTG 240
Qy 4180 CTGCTTCTGAGCTCTGCTGTGTGGATGTGGGGCCAGAGCAGCTCAGAGGAAGCC 4239
Db 241 CTGCTTCTGAGCTCTGCTGTGTGGATGTGGGGCCAGAGCAGCTCAGAGGAAGCC 300
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Db 301 AATGACAGAGTGGCCCATGTCAGTATACCTTCACTGTGCTGCTCCCATGAAATCCAGC 360
Qy 4300 TGCCAGAGCAGACCCAGCCCATGTCACTCATATTACTTACAGAGAGCAGAGCACC 4359
Db 361 TGCCAGAGCAGACCCAGCCCATGTCACTCATATTACTTACAGAGAGCAGAGCACC 420
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Db 601 GCTTACAGCAACTCTCTCCGAGACAGTCACTTCTGAGAGGAAGAGAGCACTTAAG 660
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Db 661 CAAGAAATGGAATCTGCGCAGAGGTTGGAAGACAGACCCAGAGAGTGCAGAGCTG 720
Qy 4660 AGAAGGGGCGAGTGTCCCGAGACCCAGAGCACTGCTGGGGCTGTGCGCACAGGCTCAGA 4719
Db 721 AGAAGGGGCGAGTGTCCCGAGACCCAGAGCACTGCTGGGGCTGTGCGCACAGGCTCAGA 780
Qy 4720 GAAGGT 4725
Db 781 GAAGTT 786

RESULT 12
US-08-938-669A-26
; Sequence 26, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thad D.
; APPLICANT: Polansky, Jon R.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
; PROGNOSIS AND TREATMENT OF GLAUCOMA AND
; RELATED DISEASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,669A


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/ GENERAL INFORMATION:
/ APPLICANT: NGUYEN, THAI D.
/ APPLICANT: POLANSKY, JON R.
/ APPLICANT: HUANG, WEIDONG
/ TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF
/ TITLE OF INVENTION: GLAUCOMA
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HOWREY & SIMON
/ STREET: 1299 PENNSYLVANIA AVE., N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: US
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/645,900A
/ FILING DATE: 14 MAY 1996
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MARSH, DAVID
/ REGISTRATION NUMBER: 41,408
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 383-7451
/ TELEFAX: (202) 383-6610
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1999 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-645-900A-2

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Query Match      10.7% Score 640.4; DB 2; Length 1999;
Best Local Similarity 99.8%; Pred. No. 1.8e-146;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 181 TATACCTTCAGTGTGGCCAGTCCCAATGATCCAGCTGCGCCAGAGCAGAGCCCATG 240
QY 4324 TCAAGCATCCATTAATTACAGAGACAGACAGACCAACCGTTAGACCTTGAAGGCCAC 4383
DB 241 TCAAGCATCCATTAATTACAGAGACAGACAGACCAACCGTTAGACCTTGAAGGCCAC 300
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DB 481 AAGTCAGTTCTGAGAGAGAGAGAGAGAGCTAAAGCAAGAAAATGAGAAATCTGGCCAGG 540
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DB 541 AGTTTGAAAAGACACAGCCAGAGAGGTAGCAAGGCTGAGAAAGGGGCCAGTGTCCCAAGCC 600
QY 4684 CGAGACACTGCTCGGGCTGTGTCCACCAAGGCTCCAGAGAGGT 4725
DB 601 CGAGACACTGCTCGGGCTGTGTCCACCAAGGCTCCAGAGAGGT 642

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RESULT 15
US-08-882-238A-2
Sequence 2, Application US/08882238A
Patent No. 5854415

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/ GENERAL INFORMATION:
/ APPLICANT: NGUYEN, THAI D.
/ APPLICANT: POLANSKY, JON R.
/ APPLICANT: HUANG, WEIDONG
/ TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF
/ TITLE OF INVENTION: GLAUCOMA
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HOWREY & SIMON
/ STREET: 1299 PENNSYLVANIA AVE., N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: US
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/882,238A
/ FILING DATE: 25 JUNE 1997
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MARSH, DAVID
/ REGISTRATION NUMBER: 41,408
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 383-7451
/ TELEFAX: (202) 383-6610
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1999 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-882-238A-2

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Query Match      10.7% Score 640.4; DB 2; Length 1999;
Best Local Similarity 99.8%; Pred. No. 1.8e-146;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4204 GATGTGGGGCCAGAGACAGCTCAGCTCAGAGAGCCCAATGACCAAGTGGCCGATGCCAG 4263
DB 121 GATGTGGGGCCAGAGACAGCTCAGCTCAGAGAGCCCAATGACCAAGTGGCCGATGCCAG 180
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QY      ||||| 4624 AGGTTGAGAAAGCAGAGCCAGAGGTAGCAAGGCTGAGAAAGGGGCCAGTGTCCCAAGACC 4683
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QY      ||||| 4684 CGAGACACTGTGGGCTGTGCAACCAAGGCTCCAGAGAAAGT 4725
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Job time : 958 secs

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 Db 1621 CATGCTTCTGGGCACTACTCAGCCCTGAGTGAATTGAGCTTATGCAAGACGCTGAA 1680
 Oy 1621 CATGCTTCTGGGCACTACTCAGCCCTGAGTGAATTGAGCTTATGCAAGACGCTGAA 1680
 Db 1621 CATGCTTCTGGGCACTACTCAGCCCTGAGTGAATTGAGCTTATGCAAGACGCTGAA 1680
 Oy 1681 AACCTGGAATCAGAGACTGAGTTTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1740
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 Db 1741 CGTGGCAAGTGTCTCTCTTCTCTGAGCAATGCTTCTGCTTCTGCTTCTGCTTCTG 1800
 Oy 1741 CGTGGCAAGTGTCTCTCTTCTCTGAGCAATGCTTCTGCTTCTGCTTCTGCTTCTG 1800
 Db 1741 CGTGGCAAGTGTCTCTCTTCTCTGAGCAATGCTTCTGCTTCTGCTTCTGCTTCTG 1800
 Oy 1801 GCTCTGCTTCTGAGCACTTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1860
 Db 1801 GCTCTGCTTCTGAGCACTTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1860
 Oy 1801 GCTCTGCTTCTGAGCACTTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1860
 Db 1801 GCTCTGCTTCTGAGCACTTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1860
 Oy 1861 AAGAGGCAAGCTGAGAGCTGAGCACTGAGCAAGGAGGAGTGAAGGAGGAGG 1920
 Db 1861 AAGAGGCAAGCTGAGAGCTGAGCACTGAGCAAGGAGGAGTGAAGGAGGAGG 1920
 Oy 1861 AAGAGGCAAGCTGAGAGCTGAGCACTGAGCAAGGAGGAGTGAAGGAGGAGG 1920
 Db 1861 AAGAGGCAAGCTGAGAGCTGAGCACTGAGCAAGGAGGAGTGAAGGAGGAGG 1920
 Oy 1921 CAGAGGCTGAGTCTCATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1980
 Db 1921 CAGAGGCTGAGTCTCATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1980
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 Db 2161 TGACAGAGCAAGCAAGCTCAGAGAGTGAAGTGAAGCAAGGAGTGAAGTGAAGG 2220
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 Db 2221 AAGGAGAGAGAAAGAAAGAGAGGATAGTATGAGCAAGAAAGACATTCATTCAG 2280
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 Db 2281 GGCAGTGGGAATTTGACCAAGAGATTAATGTCACGTTGCTTCTGAGAGGAGG 2340
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 Db 2281 GGCAGTGGGAATTTGACCAAGAGATTAATGTCACGTTGCTTCTGAGAGGAGG 2340
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 Oy 2341 GCTATATTTGGGGGAGAAATCAAGTCAAGGAGAGTGGGAGACCTGATTTCTAATAC 2400
 Db 2341 GCTATATTTGGGGGAGAAATCAAGTCAAGGAGAGTGGGAGACCTGATTTCTAATAC 2400
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Db 2401 TAAATTTTCTTAAAGAGTAAATTCGACCAAGTCAAGGTAATGTAACAGAGCT 2460
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Db 2581 TCAAGCTAGGTCCTGCTGACTATATGATGGTTTTTGAAGAAATCAATTCAGGATGTT 2640
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Db 2641 TACTATCTGATTGAGAAATGAGACTAGTACCCCTTGGTCAAGCTGTAACAAACACCAT 2700
Qy 2701 TTGTAATATGTCAGAGTTCAAGCTTAACTGACAGAACCAATCAATTAAGAAATAGATCTTT 2760
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Db 3001 AGTCCAGAAAGCCGTGAATTTGAATGAGGAAAAAATTAATTTGTTTTTCCACCTT 3060
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Db 3061 CTAACTAAATTTAACTTTTATTCATTCGCAATGAGCAATTAACCTCAAGAGTGTATA 3120
Qy 3121 ACAGTACCTGTGATTTTGTCAATTAACAATGAAATCAAGACATTTTATCTATTAATTA 3180
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Db 3181 GTTGTGAGATGCTGTGTAAGTGAATTTTATTAATTAATTAATTAATTAATTAATTAATTA 3240
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Db 3241 TCTGTGAGATGCTGTGTTTAAACATATTAATAAATGTTTAAATTTGATATTGTA 3300
Qy 3301 TAAATCAATTTTCAATTCATTTGTTTCTTTGTAATCTATTAATTTAATTTGAAATCA 3360
Db 3301 TAAATCAATTTTCAATTCATTTGTTTCTTTGTAATCTATTAATTTAATTTGAAATCA 3360
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Db 3421 AGTAAGAACTGATTTAGAGGCTAACTGACATTTGCTGCTGATGACAACTGAATTT 3480
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Db 3481 AGAAAGTTCTCCAAAGATACAGTTGTTTAAAGCTAGGAGTGAAGGAGGAGAAATCTGC 3540
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Db 3541 CGCTCTAATAGAAATGCTCCCTGAGAGCTGGTAGGGTCTGCTGTTGTTCTGGCTG 3600
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Db 3721 ACTAAGAAATATATCTGTTGAAATAGACACCAATAGCTCGGTATAGTGTGTAC 3780
Qy 3781 GT 3840
Db 3781 GT 3840
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Db 3961 CCAGCTCAAGTGGCCACTGTGTCTTCCCAATGAAGGCTGGCTCCCAATTAATTA 4020
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Db 4081 AGCAGAGCTTTCCAGAGGAAAGCTCAGCAAGGCTCTGCAATGAGTTCTTCTGTGACGT 4140
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Db 4141 TGTGTGAGCTTTGGGCTGAGATGCAAGCTGTCCAGCTGCTGTGCTGTGCTGTGCTGTG 4200
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Db 4201 TGGGATGTGGGGCCAGAGCAGCTCAGTCAAGAAAGGCCAATGACAGAGTGGCCGATGC 4260
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Db 4321 ATGTCAATCATCAATTAATTAAGAGAGCAGACACCAACGCTTAGACCTGAGAGGCC 4380
Qy 4381 ACCAAAGCTGCACTCAGCTCCCTGAGAGGCTCTCCACCAATTAAGCTTGAACAGGCT 4440
Db 4381 ACCAAAGCTGCACTCAGCTCCCTGAGAGGCTCTCCACCAATTAAGCTTGAACAGGCT 4440
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Qy 4501 CGGAGCAAGCTGGAACCAACCAAGAGAGTTGAGACTGCTTACAGCAACCTCTCCGA 4560
Db 4501 CGGAGCAAGCTGGAACCAACCAAGAGAGTTGAGACTGCTTACAGCAACCTCTCCGA 4560
Qy 4561 GACAAATGATGTTCTGAGAGAAAGAAAGCACTTAAGGCAAGAAATGAAATGTGAGC 4620
Db 4561 GACAAATGATGTTCTGAGAGAAAGAAAGCACTTAAGGCAAGAAATGAAATGTGAGC 4620

[illegible][illegible]

RESULT 2

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US-10-087-192-1228
Sequence 1228, Application US/10087192
Publication No. US2002018586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITILE OF INVENTION: CANCER
FILE REFERENCE: 52945200012
CURRENT APPLICATION NUMBER: US/10/087,192
PRIORITY FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1228
LENGTH: 37252
TYPE: DNA
ORGANISM: Homo sapiens
US-10-087-192-1228

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Query Match 99.6%; Score 5976.8; DB 5; Length 372521

Matches 5993; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

1 GCTCCACAGGAGTCTCCCACTTAGACTTCTGCATCAGCATGTTACAGCCAGAAGCTC 60

5946 GCTCCACAGGAGTCTCCCACTTAGACTTCTGCATCAGATGTTACAGCCAGAGCTC 6005

61 CGTGAGGGTGAGGGTCTGTGCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGC 120

6006 CGTGAGGGTGAGGCTCTGTGCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGC 6065

121 AACCTTGCCTCCAGGTTCAAGCAATCTCTGTCTCAGCCTCCGGCTAGCTGGACT 180

6066 AACCTCTGCCCTCCAGGTTCAAGCAATTCCTGTCTCAGCCTCCCGCGTAGCTGGACT 6125

181 ACAGGCGCAGCCGCTAATTTTGTATTGTTAGTAGAGATGGGTTTCACCATATTAG 240

6126 ACAGGCGCAGCCCGCTAATTTTGTATTGTTAGTAGAGATGGGTTTCACCATATTAG 6185

241 CCGGCTGCTTGAACCTCCTGACCTCAGGTGATCCACCCACTCAGCCTCCTAAAGTGC 300

6186 CCGGCTGCTTGAACCTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGC 6245

301 TGGATTACAGCATGACTCACCGCGCCCGCCAAAGGTCAGTGTTTAATAAGGAATAAC 360

6246 TGGATTACAGGCATGAGTCACCGCGCCCGCCCAAGGTCAGTGTTTAATAAGGAATAAC 6305

QY 361 TTGATGCTTTACTAAACCAAGGAAACAGACAAAGCTGTGATTAATTTCAAGGATTC 420
 Db TTGATGCTTTACTAAACCAAGGAAACAGACAAAGCTGTGATTAATTTCAAGGATTC 6365
 QY 421 TTGGGATGGGGAATGGTGGCATGAGCTGCTGCTAGTCCCAAGCACTGGTCTCTCATCA 480
 Db TTGGGATGGGGAATGGTGGCATGAGCTGCTGCTAGTCCCAAGCACTGGTCTCTCATCA 6425
 QY 481 CTTTCTCCCTCATCTCATTTTCAAGGCTAAGTTACATTTTATTCACAAAGCTTTTGTG 540
 Db CTTTCTCCCTCATCTCATTTTCAAGGCTAAGTTACATTTTATTCACAAAGCTTTTGTG 6485
 QY 541 GTAAGCTTCACATCTGTTACTGAATAAGATATACATAAATAGTTCAATTTGGGGCCA 600
 Db GTAAGCTTCACATCTGTTACTGAATAAGATATACATAAATAGTTCAATTTGGGGCCA 6545
 QY 601 TCTGTGTGTGTATAGGGGAGAGGGCATACCCAGAGACTCCTTGAAGCCCCGGGAG 660
 Db TCTGTGTGTGTATAGGGGAGAGGGCATACCCAGAGACTCCTTGAAGCCCCGGGAG 6605
 QY 661 AGGTTTCTCTCCAGCTGGGGAGCCCTGCAAGGACCCGGGGTCTGGGGTCTGAGCA 720
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 QY 841 TCTGCAGACACCAAGAGCAAAATGTGAGCAAAAGCATGACCTTACCTTCGTGGAG 900
 Db TCTGCAGACACCAAGAGCAAAATGTGAGCAAAAGCATGACCTTACCTTCGTGGAG 6786
 QY 901 GTGACAGTTTCTATGAGAAACGTGCAAGAAATTAATAGCAGCAACTTAACCA 960
 Db GTGACAGTTTCTATGAGAAACGTGCAAGAAATTAATAGCAGCAACTTAACCA 6846
 QY 961 GTGCTGAAAGAAAGAAATTAACCAATCTTGAAGATGTGGCAGCATCCTTAAACA 1020
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 QY 1021 GGCACCTGCTAGGCGCCCTGTGCTCATGAGGCCCGAGGCCCCCAAGCCGAGT 1080
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 QY 1081 CTTTCAAGCTCTCTCTCATCATGTCACAGCGCTGAGCTGCGCTGCTTCCGCTG 1140
 Db CTTTCAAGCTCTCTCTCATCATGTCACAGCGCTGAGCTGCGCTGCTTCCGCTG 7026
 QY 1141 AATGCTCTGTGTCATCTGAGCTGAGACTCTTGGCTCCAGGCTCCAGAAAGAAATG 1200
 Db AATGCTCTGTGTCATCTGAGCTGAGACTCTTGGCTCCAGGCTCCAGAAAGAAATG 7086
 QY 1201 AAGAGGAATCTAGTCTAAGGAAATCTGAGGGGAGCATGTTTCTCAAGGGAAAGG 1260
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 QY 1321 TGAAGCGGTGTGAAGGCAAGAGGTGAAGAGGCAAGGCTGAACTGCCAGATGTTCT 1380
 Db TGAAGCGGTGTGAAGGCAAGAGGTGAAGAGGCAAGGCTGAACTGCCAGATGTTCT 7266
 QY 1381 AGTGTGTTCACAGGGGCTGGAGGTTTTCGTTGCTTCGTGAGCCTTTTATCTTTTCT 1440
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 QY 1621 CATGCTTGGGCAACTATCAGCCCTGTGGTGAAGCTTGGCTTATAGCAAGCGTCCGA 1680
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 QY 1801 GCTCTGTGTCTGTGAACATTTCCCTGTGATTTCTGTGAGGGGGATGTTGAGAGGG 1860
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 QY 7746 GCTCTGTGTGTGTGAACATTTCCCTGTGATTTCTGTGAGGGGGATGTTGAGAGGG 7805
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 QY 1981 CAATGCTCAGAAAGCTCAATGAACCCCAAGCCCAATTTCTTCCCTAAGCATAGAC 2040
 Db CAATGCTCAGAAAGCTCAATGAACCCCAAGCCCAATTTCTTCCCTAAGCATAGAC 7926
 QY 7926 CAATGCTCAGAAAGCTCAATGAACCCCAAGCCCAATTTCTTCCCTAAGCATAGAC 7985
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 QY 2221 AAGGAGAGAGAAAGAAAGAGAGATGATATAGCAAGAAAGACAGATTCAATCAAG 2280
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 QY 2401 TATATTTTCTTTTCAAGAGTGAATTTGAGCAAGTCAAGAGTGAATGAGGCT 2460
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 QY 2461 GTAAGATTAATTAAGTTTCTCTTATTAAGAACTCTTTTCTGTGAGATTAGCAGCA 2520
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 QY 2521 AGGCAATCCGTTCTTTTAAAGAGAAACATCTCTAAGAGTAAAGCAACAGAT 2580

D	8466	AGGGCAATCCCGTTCTTTTAAACAGAAAGAAAACATTCCTAAGATTAACCCAAACAGAT	8525
Q	2581	TCAAGCCTAGGCTCTGCTGACTATATGATGGTTTTTGAAAAATCATTTCAAGCATGTT	2640
D	8526	TCAAGCCTAGGCTCTGCTGACTATATGATGGTTTTTGAAAAATCATTTCAAGCATGTT	8585
Q	2641	TACTATCTGATTCAGAAAAATGAGCTAGTACCCTTTGGTCAAGCTGTAAACAAACCCAT	2700
D	8586	TACTATCTGATTCAGAAAAATGAGCTAGTACCCTTTGGTCAAGCTGTAAACAAACCCAT	8645
Q	2701	TTGTAAATGCTCAAGTTCAAGCTTAACCTGACAGAACCAATCAATATAGAAATGAACTTT	2760
D	8646	TTGTAAATGCTCAAGTTCAAGCTTAACCTGACAGAACCAATCAATATAGAAATGAACTTT	8705
Q	2761	AGAGCAAACTGNGTTTCTCACTCGAGAGTGAAGTCTGCCAGGCAAGTTTGAAATATTT	2820
D	8706	AGAGCAAACTGNGTTTCTCACTCGAGAGTGAAGTCTGCCAGGCAAGTTTGAAATATTT	8765
Q	2821	ACTTCACAAGTATGACACTGTTGGTATTAACAATTAAGTGTCAAGGCAATC	2880
D	8766	ACTTCACAAGTATGACACTGTTGGTATTAACAATTAAGTGTCAAGGCAATC	8825
Q	2881	ATTATTTCAAGGCGCTTAAAGTTACTTCTGACGTTTTGGATATTTATGGCTATGGCC	2940
D	8826	ATTATTTCAAGGCGCTTAAAGTTACTTCTGACGTTTTGGATATTTATGGCTATGGCC	8885
Q	2941	ATTGCTTTTGTGTTTTCTCTTGGGTTTATATGTAAACAGGATATTAACCTAC	3000
D	8886	ATTGCTTTTGTGTTTTCTCTTGGGTTTATATGTAAACAGGATATTAACCTAC	8945
Q	3001	AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAATTACATTTTGTTTTACACCTT	3060
D	8946	AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAATTACATTTTGTTTTACACCTT	9005
Q	3061	CTAATCTAAATTTAATGATTTATTCATGGAATGAGCCATAACCTCAAGTGGTATA	3120
D	9006	CTAATCTAAATTTAATGATTTATTCATGGAATGAGCCATAACCTCAAGTGGTATA	9065
Q	3121	ACAGTACCTGTGATTTGTTCATTAACCATAGAAATCAGACATTTTATCTATATTACA	3180
D	9066	ACAGTACCTGTGATTTGTTCATTAACCATAGAAATCAGACATTTTATCTATATTACA	9125
Q	3181	GTGTGTGACAGATAGCTGTGAAGTGAATATTTATCTCAAAACCTACTTTGAAATTAGCC	3240
D	9126	GTGTGTGACAGATAGCTGTGAAGTGAATATTTATCTCAAAACCTACTTTGAAATTAGCC	9185
Q	3241	TCCCTGCTGATCTCTGTTTTTAAACATTTAATPAAAACATGTTTAAATTTTATTTTGA	3300
D	9186	TCCCTGCTGATCTCTGTTTTTAAACATTTAATPAAAACATGTTTAAATTTTATTTTGA	9245
Q	3301	TAAATCAATTTCAATATCATCTTGTCTCTTGTATCTATATTTTATATTTGAAAACA	3360
D	9246	TAAATCAATTTCAATATCATCTTGTCTCTTGTATCTATATTTTATATTTGAAAACA	9305
Q	3361	TCTTTCTGAGAAAGTTCGCCAGATTTTCACAATGAGGTTCTTGGCATGACACACACAG	3420
D	9306	TCTTTCTGAGAAAGTTCGCCAGATTTTCACAATGAGGTTCTTGGCATGACACACACAG	9365
Q	3421	AGTAAAGACTGATTTTATGAGGCTTAACATTTGACATTTGTGCTGAGATGCAACATGGAATT	3480
D	9366	AGTAAAGACTGATTTTATGAGGCTTAACATTTGACATTTGTGCTGAGATGCAACATGGAATT	9425
Q	3481	AGAAAGTTCTCCCAAAAGATACAGATGTTTTTAAAGCTAAGGGGTAGAGGGGGAATCTGC	3540
D	9426	AGAAAGTTCTCCCAAAAGATACAGATGTTTTTAAAGCTAAGGGGTAGAGGGGGAATCTGC	9485
Q	3541	CGTTTCTATAGAAATGCTCTCCCTGGAAGCTGTGAAGGTGCTGTCCTTGTGTCTGCTG	3600
D	9486	CGTTTCTATAGAAATGCTCTCCCTGGAAGCTGTGAAGGTGCTGTCCTTGTGTCTGCTG	9545
Q	3601	GCTGTATTTTCTCTGTCCTGCTGCTACAGTCTTAAAGACTTGTTTGATCTCAAGTCTCT	3660
D	9546	GCTGTATTTTCTCTGTCCTGCTGCTACAGTCTTAAAGACTTGTTTGATCTCAAGTCTCT	9605

[illegible]

QY	4741	GGGAGCTCTGAGTTGAGAGGGGATGATGGCTGGATAGGACCTGGTACAGAGCGCTCCAGGC	4800
Db	10666	GGGAGCTCTGAGTTGAGAGGGGATGATGGCTGGATAGGACCTGGTACAGAGCGCTCCAGGC	10744
QY	4801	CTCCCTGCTGCTCTTCTCTCTAGAGCTGACAGCTAGCACAAGACAGATGAAATTAGG	4860
Db	10746	CTCCCTGCTGCTCTTCTCTCTAGAGCTGACAGCTAGCACAAGACAGATGAAATTAGG	10800
QY	4861	AAAGCAGAGCGATCACCTTCAAGTATTACTAGTAATTTAGTCTGTAGAGCTTCAATTAG	4920
Db	10806	AAAGCAGAGCGATCACCTTCAAGTATTACTAGTAATTTAGTCTGTAGAGCTTCAATTAG	10866
QY	4921	ATTAGTGGTCAAGATCTTGTGGCCCTCCATGTCAGTTTTCACATGCCATAGCAAAAG	4980
Db	10866	ATTAGTGGTCAAGATCTTGTGGCCCTCCATGTCAGTTTTCACATGCCATAGCAAAAG	10922
QY	4981	AGAAATAAAGACCCGGGTGAGATGTGTCTCATATGACAGTATGAAAGTTTCAATTGT	5040
Db	10926	AGAAATAAAGACCCGGGTGAGATGTGTCTCATATGACAGTATGAAAGTTTCAATTGT	10988
QY	5041	CCCTTTGAAAAAATACTATCTTTTGTGAACCTTTGCTCAGATGTGTAATTTGTACCTTTGA	5100
Db	10986	CCCTTTGAAAAAATACTATCTTTTGTGAACCTTTGCTCAGATGTGTAATTTGTACCTTTGA	11045
QY	5101	TGTTAAATATGACCTTTAATTAATGAATTAACAATGATTTGGGAAATATATATAGTGTAT	5160
Db	11046	TGTTAAATATGACCTTTAATTAATGAATTAACAATGATTTGGGAAATATATATAGTGTAT	11105
QY	5161	AGTTTGTATTATTTTAAATATGTCTTCCCTGGCAAAATPAAGAGATGGACCTCTGT	5220
Db	11106	AGTTTGTATTATTTTAAATATGTCTTCCCTGGCAAAATPAAGAGATGGACCTCTGT	11165
QY	5221	CAGTTTCTTAATATATGTTGTTCTGAAAGTTTCTTACTCAGTCCAAATCTGAGAACCTCTG	5280
Db	11166	CAGTTTCTTAATATATGTTGTTCTGAAAGTTTCTTACTCAGTCCAAATCTGAGAACCTCTG	11225
QY	5281	CTTTTAAGTCATCAGACAAATCTTGAGATGAGCTTTTCTGAAGGCTCTTCTGTTCATC	5340
Db	11226	CTTTTAAGTCATCAGACAAATCTTGAGATGAGCTTTTCTGAAGGCTCTTCTGTTCATC	11285
QY	5341	CTGTGCTCTTCTTACCTAAAGGTGAGCTGTGTGTGTGTGTGGGG--GGGTGGGGGGGTGA	5398
Db	11286	CTGTGCTCTTCTTACCTAAAGGTGAGCTGTGTGTGTGTGTGGGGGGGGGGGGGGGA	11345
QY	5399	GGTGTGGGGGAGGTCTTCTTAATAGCTGGGAAGATGTAATTTGTGTCACTTTTGTGAA	5458
Db	11346	GGTGTGGGGGAGGTCTTCTTAATAGCTGGGAAGATGTAATTTGTGTCACTTTTGTGAA	11405
QY	5459	AGTGGGCTCCCAATATATCCCTGTGTGAGAAAGTGTCTAATCATGAGAAATAGCAAC	5518
Db	11406	AGTGGGCTCCCAATATATCCCTGTGTGAGAAAGTGTCTAATCATGAGAAATAGCAAC	11465
QY	5519	AAATCCAGTTGTGGAACAATTAATGTTTGGACTGTGCAAAAGTGTCACTGTGCAAGAA	5578
Db	11466	AAATCCAGTTGTGGAACAATTAATGTTTGGACTGTGCAAAAGTGTCACTGTGCAAGAA	11525
QY	5579	GAAGAAAGGGGTGGGGAAGGCTGTGTCTAATTAATTAAGACCTAAAGAAATGTGTTAAC	5638
Db	11526	GAAGAAAGGGGTGGGGAAGGCTGTGTCTAATTAATTAAGACCTAAAGAAATGTGTTAAC	11585
QY	5639	AAATGTATGTCATATAGTCTTGAATTTGGTGTCTTATCATCAAGGGGGAAAAAGCTATGAGA	5698
Db	11586	AAATGTATGTCATATAGTCTTGAATTTGGTGTCTTATCATCAAGGGGGAAAAAGCTATGAGA	11645
QY	5699	ACAGTATTGGGATPAACATGAGCAATTGACTGTCAATTAATGTAATGTAATGTAATGTT	5758
Db	11646	ACAGTATTGGGATPAACATGAGCAATTGACTGTCAATTAATGTAATGTAATGTAATGTT	11705
QY	5759	CAGTTTCTTGATGATATATGATACTGTGGTTGCGAAGATTAATAATCTTGTGTTATGGA	5818
Db	11706	CAGTTTCTTGATGATATATGATACTGTGGTTGCGAAGATTAATAATCTTGTGTTATGGA	11765
QY	5819	GATCATGCTTAATGATACCCAGGGGTAGGGCTCAGAGTGTCTGCATTTGCTCTCAATGTG	5878

[illegible]

Db 1576 TTGAATGGTTACTTAAACCAAGGAAAAAGACAAAAGCTGTGATTAATTTCAAGGAATTC 1635
 Oy 421 TTGGATGGGGAATGGTSCCATGAGCTGCGCTGAGCCGACACCACTGGTCCCATCA 480
 Db 1636 TTGGATGGGGAATGGTSCCATGAGCTGCGCTGAGCCGACACCACTGGTCCCATCA 1695
 Oy 481 CTTCCTTCCTCATCTCATTTTTCAGGCTAAGTTACATTTTATTCACACATGCTTTTGTG 540
 Db 1696 CTTCCTTCCTCATCTCATTTTTCAGGCTAAGTTACATTTTATTCACACATGCTTTTGTG 1755
 Oy 541 GTAAAGCTTCACATCTGTTACTGAATAATAGATATACATAAACCTAGTTCACTTTGGGGCA 600
 Db 1756 GTAAAGCTTCACATCTGTTACTGAATAATAGATATACATAAACCTAGTTCACTTTGGGGCA 1815
 Oy 601 TCTGTGTGTGTATAGGGGAGAGAGGATACCCGAGAGACTCTTGAAGCCCCGGGAG 660
 Db 1816 TCTGTGTGTGTATAGGGGAGAGAGGATACCCGAGAGACTCTTGAAGCCCCGGGAG 1875
 Oy 661 AGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTTGGGTGTCTGAGCA 720
 Db 1876 AGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTTGGGTGTCTGAGCA 1935
 Oy 721 ACTTCCAGCCCGTGCACCTGGTTGTTTGTATATCACTCTCTAGGAGCCTGTGCTTTCT 780
 Db 1936 ACTTCCAGCCCGTGCACCTGGTTGTTTGTATATCACTCTCTAGGAGCCTGTGCTTTCT 1995
 Oy 781 ATTTCTGTGTGACTGGTTCAATTCACTCAAGGCACTTCACTTGAACAATTTATAGTACTTATA 840
 Db 1996 ATTTCTGTGTGACTGGTTCAATTCACTCAAGGCACTTCACTTGAACAATTTATAGTACTTATA 2055
 Oy 841 TCTGCAAGACACAGAGACAAAATGTGAGCAAGACAGTCACTGCCCTTACCTTCGTGAG 900
 Db 2056 TCTGCAAGACACAGAGACAAAATGTGAGCAAGACAGTCACTGCCCTTACCTTCGTGAG 2115
 Oy 901 GTGACAGTTTCTCATAGGAAGAGCTGACAGAGAAAATTATAGCCAGCCACTTAAACCA 960
 Db 2116 GTGACAGTTTCTCATAGGAAGAGCTGACAGAGAAAATTATAGCCAGCCACTTAAACCA 2175
 Oy 961 GTGCTGAAGAAAGAAATTAACACATCTTGAGAAATTGTGCGAGACATCCCTTAACA 1020
 Db 2176 GTGCTGAAGAAAGAAATTAACACATCTTGAGAAATTGTGCGAGACATCCCTTAACA 2235
 Oy 1021 GGCACACTCCCTAGAGCCCCCTGCTGCTCATCTGTGCCGAGAGCCCCCAAGCCGAGT 1080
 Db 2236 GGCACACTCCCTAGAGCCCCCTGCTGCTCATCTGTGCCGAGAGCCCCCAAGCCGAGT 2295
 Oy 1081 CTTCAGAGCTCTCTCTCATATGTCACAGCGCTGAGAGTGGCTGCTGCTTCCCTGTG 1140
 Db 2296 CTTCAGAGCTCTCTCTCATATGTCACAGCGCTGAGAGTGGCTGCTGCTTCCCTGTG 2355
 Oy 1141 AATGCTCCGTGATCTGAGAGCTGGAGACTCCTTGCTCAGGCTCCAGAAAGAAATGG 1200
 Db 2356 AATGCTCCGTGATCTGAGAGCTGGAGACTCCTTGCTCAGGCTCCAGAAAGAAATGG 2415
 Oy 1201 AGAGGAAAACCTAGTCTAACGAGAAATCTGAGAGGGGACAGTGTTCCTCAGAGGAAAAGG 1260
 Db 2416 AGAGGAAAACCTAGTCTAACGAGAAATCTGAGAGGGGACAGTGTTCCTCAGAGGAAAAGG 2475
 Oy 1261 GCTCCACGTCCTCAAGAGAAATTCAGAGAGGTGGGACTGCAAGGAGGTGGGAGCGCTGGGCG 1320
 Db 2476 GCTCCACGTCCTCAAGAGAAATTCAGAGAGGTGGGAGTGCAGAGGAGGTGGGAGCGCTGGGCG 2535
 Oy 1321 TGAAGCGGGTCTGAAGGAGAGAGGTGAAGAGGAGCAAGCTGAGAGCTCCAGAGTGTTC 1380
 Db 2536 TGAAGCGGGTCTGAAGGAGAGAGGTGAAGAGGAGCAAGCTGAGAGCTCCAGAGTGTTC 2595
 Oy 1381 AGTGTGTTCACGGGCTGAGAGTTTCGGTGTCTCTGTGAGCCTTTTATCTTTTCT 1440
 Db 2596 AGTGTGTTCACGGGCTGAGAGTTTCGGTGTCTCTGTGAGCCTTTTATCTTTTCT 2655
 Oy 1441 CTGCTTGAAGAGAGAAAGTCTATTTTCATGAGAGGATGAGATTCAATAAGTCAAGCTGTT 1500
 Db 2656 CTGCTTGAAGAGAGAAAGTCTATTTTCATGAGAGGATGAGATTCAATAAGTCAAGCTGTT 2715

Oy 1501 AAAATTCAGAGGTGTGATGGGTTTTCCTTACAGAAAGCCTTATTTATGGGAATATAG 1560
 Db 2716 AAAATTCAGAGGTGTGATGGGTTTTCCTTACAGAAAGCCTTATTTATGGGAATATAG 2775
 Oy 1561 GAAGCGAGCTCATTTCTAGGCGCTTAATTCACGGAAGAGTGACTGAAGCTTTTCTTT 1620
 Db 2776 GAAGCGAGCTCATTTCTAGGCGCGTAAATTCACGGAAGAGTGACTGAAGCTTTTCTTT 2835
 Oy 1621 CATGCTTCTGGGCACTATCTCAGCCGTGTGTGACTGTGAGCTATGCAAGAAGGTGAA 1680
 Db 2836 CATGCTTCTGGGCACTATCTCAGCCGTGTGTGAGACTGTGAGCTTATGCAAGAAGGTGAA 2895
 Oy 1681 AACCTTGAATCAGAGACTCGATTTTCTTCTGTGTTCTGCAATGTGCTGTGCGAC 1740
 Db 2896 AACCTTGAATCAGAGACTCGATTTTCTTCTGTGTTCTGCAATGTGCTGTGCGAC 2955
 Oy 1741 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATATCTTCTGCTATTAAGACCTTGCA 1800
 Db 2956 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATATCTTCTGCTATTAAGACCTTGCA 3015
 Oy 1801 GCTCTCGTGTCTGTGAACCTTCCCTGTGATTCCTGTGAGGGGGATGTTGAGAGGG 1860
 Db 3016 GCTCTCGTGTCTGTGAACCTTCCCTGTGATTCCTGTGAGGGGGATGTTGAGAGGG 3075
 Oy 1861 AAGAGGCAAGCTGAGAGCACTGAGCCACAGGGAGGTGAGGGGACAGAAAGCAGG 1920
 Db 3076 AAGAGGCAAGCTGAGAGCACTGAGCCACAGGGAGGTGAGGGGACAGAAAGCAGG 3135
 Oy 1921 CAGAAAGTGGTGTCTCATAGTCTCTCACTGTATACGTCAAGACTCCAGAACCGGAGCA 1980
 Db 3136 CAGAAAGTGGTGTCTCATAGTCTCTCACTGTATACGTCAAGACTCCAGAACCGGAGCA 3195
 Oy 1981 CAATGCTTCAGAAAGCTCAATGAACCAACAGCCACTTTCTTCCCTAAGATAGAC 2040
 Db 3196 CAATGCTTCAGAAAGCTCAATGAACCAACAGCCACTTTCTTCCCTAAGATAGAC 3255
 Oy 2041 AATGCAATTTTCCATATACCAAAAAGAAATGACAGAGACTAATGATGATGCTTTGCTG 2100
 Db 3256 AATGCAATTTTCCATATACCAAAAAGAAATGACAGAGACTAATGATGATGCTTTGCTG 3315
 Oy 2101 GCATTCAAAACTGGGCGACAGACAGTGGAAAATGCCAGAAATGTTTAACTTTTCAACC 2160
 Db 3316 GCATTCAAAACTGGGCGACAGACAGTGGAAAATGCCAGAAATGTTTAACTTTTCAACC 3375
 Oy 2161 TGAACGAGACCCCAAGCAAGCTCAGAGATGACTGTGACAGGACGGAAGTCACTGAGGCG 2220
 Db 3376 TGAACGAGACCCCAAGCAAGCTCAGAGATGACTGTGACAGGACGGAAGTCACTGAGGCG 3435
 Oy 2221 AGGAGAGAGAAAGAAAAGAGAGGATAGTATAGACAGAAAGACAGATTCAATCAAG 2280
 Db 3436 AGGAGAGAGAAAGAAAAGAGAGGATAGTATAGACAGAAAGACAGATTCAATCAAG 3495
 Oy 2281 GGCAGTGGAAATTCACACAGGATTAATATGTCACGTATCTGTGTTCTAGAGGCGAG 2340
 Db 3496 GGCAGTGGAAATTCACACAGGATTAATATGTCACGTATCTGTGTTCTAGAGGCGAG 3555
 Oy 2341 GCTATATGTGGGGGAAAAAATCAGTTCAGAGGAAGTCGGGAGACTGATTTCTAATAC 2400
 Db 3556 GCTATATGTGGGGGAAAAAATCAGTTCAGAGGAAGTCGGGAGACTGATTTCTAATAC 3615
 Oy 2401 TATATTTTCTTTTCAAGCTGAGTAATCTGAGCAATGTCANAGTATGTAACAGGCT 2460
 Db 3616 TATATTTTCTTTTCAAGCTGAGTAATCTGAGCAATGTCANAGTATGTAACAGGCT 3675
 Oy 2461 GTAAGATTAATTAAGTTTCTCTTATTAAGAACTTTTCTGTGTGAGTTAGCAGCA 2520
 Db 3676 GTAAGATTAATTAAGTTTCTCTTATTAAGAACTTTTCTGTGTGAGTTAGCAGCA 3735
 Oy 2521 AGGCAATCCGCTTCTTTTAAACAGAGAAAGAACTTCTTAAGATTAAGCAACAGT 2580
 Db 3736 AGGCAATCCGCTTCTTTTAAACAGAGAAAGAACTTCTTAAGATTAAGCAACAGT 3795

OY	2581	TCAACCCTAGGCTCTGCACTATATGATGTGTTTTGGAAAAATCATTTTCAAGCAATGTT	2640
Db	3796	TCAACCCTAGGCTCTGCACTATATGATGTGTTTTGGAAAAATCATTTTCAAGCAATGTT	3855
OY	2641	TACTATCTGATTCAGAAAATGAGACTAGTACCCCTTGGCTAGCTGTAAACAACCCCAT	2700
Db	3856	TACTATCTGATTCAGAAAATGAGACTAGTACCCCTTGGCTAGCTGTAAACAACCCCAT	3915
OY	2701	TTGTAAATGTCTCAAGTTCAAGCTTAACTGCAAGCAACCATCAAAATAGAAATGATCTTT	2768
Db	3916	TTGTAAATGTCTCAAGTTCAAGCTTAACTGCAAGCAACCATCAAAATAGAAATGATCTTT	3974
OY	2761	AGAGGAACCTGTGTTTCTCCAC-TCTGAGGTGAGTCTGCCAGGCACTTTGGAAATATT	2819
Db	3975	AGAGGAACCTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGCACTTTGGAAATATT	4034
OY	2820	TACTTCACAAGATTTGACACTGTGTTGGATTTAAACAATAAAGTGTCTCAAAAGGCAAT	2879
Db	4035	TACTTCACAAGATTTGACACTGTGTTGGATTTAAACAATAAAGTGTGTCTCAAAAGGCAAT	4094
OY	2880	CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTTGGCTATTCG	2939
Db	4095	CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTTGGCTATTCG	4154
OY	2940	CATTGTCTTTTGTGTTTTCTCTTGGGTTATTATGTAAAGAGGGATTTATPACCTA	2999
Db	4155	CATTGTCTTTTGTGTTTTCTCTTGGGTTATTATGTAAAGAGGGATTTATPACCTA	4214
OY	3000	CAGTCCAGAAAGCCGTGAATTTGAAATAGAGAAAAAATTACATTTTGTGTTTACCCCT	3059
Db	4215	CAGTCCAGAAAGCCGTGAATTTGAAATAGAGAAAAAATTACATTTTGTGTTTACCCCT	4274
OY	3060	TCTAATAAATTTAAACATTTTATTCATTCGGAATAGAGCACTAACTCAAGTGGAT	3119
Db	4275	TCTAATAAATTTAAACATTTTATTCATTCGGAATAGAGCACTAACTCAAGTGGAT	4334
OY	3120	AACAGTACCTGTGATTTGTGCAATACCAATAGAAATCAAGACATTTTATCTATTTAC	3179
Db	4335	AACAGTACCTGTGATTTGTGCAATACCAATAGAAATCAAGACATTTTATCTATTTAC	4394
OY	3180	AGTGTGACATPCCGTGTAGGAAATATTTTATCTCAAACTACTTTGAAATTTAGAC	3239
Db	4395	AGTGTGACATPCCGTGTAGGAAATATTTTATCTCAAACTACTTTGAAATTTAGAC	4454
OY	3240	CTCCTGCTGATCTGTTTTTAAACATATTAATAAAACATGTTTAAATTTTGATATTG	3299
Db	4455	CTCCTGCTGATCTGTTTTTAAACATATTAATAAAACATGTTTAAATTTTGATATTG	4514
OY	3300	ATAATCATATTTCAATATCATTTGTTCTTGTGTAATCTATATTTATATTTTGAANAAC	3359
Db	4515	ATAATCATATTTCAATATCATTTGTTCTTGTGTAATCTATATTTATATTTTGAANAAC	4574
OY	3360	ATCTTTCTGAGAAAGTTCGCCAGATTTACCAATGAGGTTCTTGGCATGCAACAACA	3419
Db	4575	ATCTTTCTGAGAAAGTTCGCCAGATTTCAACAAATGAGGTTCTTGGCATGCAACAACA	4634
OY	3420	GAGTAAAGAACTGATTTAGAGGCTAACATTTGACATTTGGCTCGATGAGCAAGCTGAAT	3479
Db	4635	GAGTAAAGAACTGATTTAGAGGCTAACATTTGACATTTGGCTCGATGAGCAAGCTGAAT	4694
OY	3480	TAGAAAGTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAAATCTG	3539
Db	4695	TAGAAAGTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAAATCTG	4754
OY	3540	CCGCTTCTATAGGAATGCTCTTCCCTGAGACCTGGTAGGGTCTGTCTTGTGTTCTGGCT	3599
Db	4755	CCGCTTCTATAGGAATGCTCTTCCCTGAGACCTGGTAGGGTCTGTCTTGTGTTCTGGCT	4814
OY	3600	GGCTGTATATTTTCTCTGTCCCTCTACAGTCTTAAAGAACTGTTTGGATCTCCAGTTCC	3659
Db	4815	GGCTGTATATTTTCTCTGTCCCTCTACAGTCTTAAAGAACTGTTTGGATCTCCAGTTCC	4874
OY	3660	TAGCATATGTGCTCGACAAGTCAAGTGTCTCAATGAGTTTGCACAGTGAATGAAAAATTA	3719

[illegible]

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Db      5955 TGGGGGAGCTGAGTTCAGCAGGTATATGCTGTAGTACCTGTCAAGCGCTCCA 6014
Qy      4798 GGCCTCCCTGCTGCTCTTCTCTAGAGACTGCACAGTACAGACAGATGAATTA 4857
Db      6015 GGCCTC---CCTGCGCTTCTCTAGAGACTGCACAGTACAGACAGATGAATTA 6070
Qy      4858 AGGAAAGCAGCAGATCACTTCAAGTATTAAGTAAATTTAGCTCTGAGAGCTTCAT 4917
Db      6071 AGGAAAGCACA-CGATCACTTCAAGTATTAAGTAAATTTAGCTCTGAGAGCTTCAT 6129
Qy      4918 TAGATTAGTGTTCAGAGTCTTGTGCCCCCTCAAGTCAG 4957
Db      6130 TAGATTAGTGTTCAGAGTCTTGTGCCCCCTCAAGTCAG 6169

RESULT 4
US-09-985-637A-1
/ Sequence 1, Application US/09985637A
/ Publication No. US20030119000A1
/ GENERAL INFORMATION:
/ APPLICANT: Polansky, Jon
/ TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PRO
/ TITLE OF INVENTION: TO DEVELOP GLAUCOMA
/ FUND REFERENCE: 13587.296
/ CURRENT APPLICATION NUMBER: US/09/985,637A
/ CURRENT FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 5300
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-985-637A-1

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Query Match 67.8%; Score 4069.4; DB 3; Length 5300;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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Qy      1 GCTCCACAGAAAGTCTCCCACTCTAGACTTCTGCATCGATGTTTACAGCCAGAAAGTC 60
Db      1216 GCTCCACAGAAAGTCTCCCACTCTAGACTTCTGCATCGATGTTTACAGCCAGAAAGTC 1275
Qy      61 CGTGAAGGTGAGGGTCTGTGTCTTACACCTTACCTGTATGCTTACACCTGAGCTCACTGC 120
Db      1276 CGTGAAGGTGAGGGTCTGTGTCTTACACCTTACCTGTATGCTTACACCTGAGCTCACTGC 1335
Qy      121 AACCTTGTCTCCCAAGTTCAGCAATCTCTGTCTCAGCCTCCCGCTAGCTGGAGT 180
Db      1336 AACCTTGTCTCCCAAGTTCAGCAATCTCTGTCTCAGCCTCCCGCTAGCTGGAGT 1395
Qy      181 ACAGGCGACGCCCGGCTAATTTTGTATTTAGTATGAGATGGGGTTTACCATATTAG 240
Db      1396 ACAGGCGACGCCCGGCTAATTTTGTATTTAGTATGAGATGGGGTTTACCATATTAG 1455
Qy      241 CCGGCTGTGCTTTGAATCTCTGAACCTCAGGTGATCCACCCACCTCAGCTCTTAAAGTGC 300
Db      1456 CCGGCTGTGCTTTGAATCTCTGAACCTCAGGTGATCCACCCACCTCAGCTCTTAAAGTGC 1515
Qy      301 TGGGATTAACAGGATAGTCAACCGCGCCCGGCCAAGGCTCAGTGTATTAAGAAATAC 360
Db      1516 TGGGATTAACAGGATAGTCAACCGCGCCCGGCCAAGGCTCAGTGTATTAAGAAATAC 1575
Qy      361 TGGATGTGTTTACTAAACCAACAGGAAACAGACAAAGCTGTGATATTTTCAGGGAATTC 420
Db      1576 TGGATGTGTTTACTAAACCAACAGGAAACAGACAAAGCTGTGATATTTTCAGGGAATTC 1635
Qy      421 TTGGAGTGGGGAATGTGTCATAGTGCCTGTGCTTACGCCACCACTGCTCTCATCA 480
Db      1636 TTGGAGTGGGGAATGTGTCATAGTGCCTGTGCTTACGCCACCACTGCTCTCATCA 1695
Qy      481 CTTTCTTCCCTCATCTCTCATTTTTCAGGCTTAAGTATTAATTTTACCAATGCTTTTGTG 540
Db      1696 CTTTCTTCCCTCATCTCTCATTTTTCAGGCTTAAGTATTAATTTTACCAATGCTTTTGTG 1755

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Qy      541 GTAAGCTTCACATCGTTACTGAATAATAGATATACATAAATAGTTCCATTTTGGGGCCA 600
Db      1756 GTAAGCTTCACATCGTTACTGAATAATAGATATACATAAATAGTTCCATTTTGGGGCCA 1815
Qy      601 TCTGTGTGTGTGTATAGGGAGAGAGGGCATTCGCCAGAGACTCTTGAAGCCCCCGGAG 660
Db      1816 TCTGTGTGTGTGTATAGGGAGAGAGGGCATTCGCCAGAGACTCTTGAAGCCCCCGGAG 1875
Qy      661 AGGTTTCCCTTCAGAGTGGGGAGAGCCCTGCAGAGACCCGGGGGTCTGGGTCTCTGAGCA 720
Db      1876 AGGTTTCCCTTCAGAGTGGGGAGAGCCCTGCAGAGACCCGGGGGTCTGGGTCTCTGAGCA 1935
Qy      721 ACTGCGAGCCCGTGCACCTGCTGTGTTTGTATCACTCTGAGGACCTGTGCTTCT 780
Db      1936 ACTGCGAGCCCGTGCACCTGCTGTGTTTGTATCACTCTGAGGACCTGTGCTTCT 1995
Qy      781 ATTTCTGTGTGATCTGCTTCAATTCACAGGATTCATGACAAATTTATGAGTACTTATA 840
Db      1996 ATTTCTGTGTGATCTGCTTCAATTCACAGGATTCATGACAAATTTATGAGTACTTATA 2055
Qy      841 TCTGCAGACACACAGACAAATGTGAGCAAGAGTCACTGCGCTTACCTTGGTGGAG 900
Db      2056 TCTGCAGACACACAGACAAATGTGAGCAAGAGTCACTGCGCTTACCTTGGTGGAG 2115
Qy      901 GTGACAGTTTCTCATGGAAGACGTGCAGAGAAATTTATAGCCAGCCACTTAAACCCA 960
Db      2116 GTGACAGTTTCTCATGGAAGACGTGCAGAGAAATTTATAGCCAGCCACTTAAACCCA 2175
Qy      961 GTGCGAAAGAAAGAAATTAACACATCTTGAAGAAATTTGGCCAGAGATCCCTTAACAA 1020
Db      2176 GTGCGAAAGAAAGAAATTAACACATCTTGAAGAAATTTGGCCAGAGATCCCTTAACAA 2235
Qy      1021 GGGCAACCTCCCTAGAGCCCGCTGCTGCTCATGCTGTCGCGAGAGCCCGCAAGCCGAGT 1080
Db      2236 GGGCAACCTCCCTAGAGCCCGCTGCTGCTCATGCTGTCGCGAGAGCCCGCAAGCCGAGT 2295
Qy      1081 CTTCCAGACCTCTCTCTCCATCAGTCAAGGCTGCAGACTGAGCTGCTGCTTCCCGTGT 1140
Db      2296 CTTCCAGACCTCTCTCTCCATCAGTCAAGGCTGCAGACTGAGCTGCTGCTTCCCGTGT 2355
Qy      1141 AATGCTCTGTGATCTGAGCTGAGAGACTCTTGTGCTCCAGGCTCCAGAAAGAAATAG 1200
Db      2356 AATGCTCTGTGATCTGAGCTGAGAGACTCTTGTGCTCCAGGCTCCAGAAAGAAATAG 2415
Qy      1201 AGAGGAAACTAGTCTAACGAGAAATCGAGGGGACAGTGTCTCTCAGAGGGGAAAGG 1260
Db      2416 AGAGGAAACTAGTCTAACGAGAAATCGAGGGGACAGTGTCTCTCAGAGGGGAAAGG 2475
Qy      1261 GCTTCCAGTCCAGAGAAATTCAGAGAGTGGGACCTGCAGAGATGGGAGACGCTGGGGC 1320
Db      2476 GCTTCCAGTCCAGAGAAATTCAGAGAGTGGGACCTGCAGAGATGGGAGACGCTGGGGC 2535
Qy      1321 TGAAGCGGTGCTGAAGGACAGAGAGTGAAGAGGCAAGCTGGAAGCTGCCAATGTTTC 1380
Db      2536 TGAAGCGGTGCTGAAGGACAGAGAGTGAAGAGGCAAGCTGGAAGCTGCCAATGTTTC 2595
Qy      1381 AGTGTGTTTACAGGGGCTGGGAGTTTTCGTTGCTCTGCTGAGGCTTTTATCTTTTCT 1440
Db      2596 AGTGTGTTTACAGGGGCTGGGAGTTTTCGTTGCTCTGCTGAGGCTTTTATCTTTTCT 2655
Qy      1441 CTGCTTGAAGAGAGAAAGTCTATTTCAATGAAGGATCAGTTTCAATAAGCTCAGCTGT 1500
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[illegible][illegible]

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Qy 1381 AGTGTGTTCAAGGGCTGGAGTTTCGGTGTCTCTGTAGGCTTTTATCTTTCT 1440
Db 2596 AGTGTGTTCAAGGGCTGGAGTTTCGGTGTCTCTGTAGGCTTTTATCTTTCT 2655
Qy 1441 CTGCTTGAAGAGAAAGTCTATTCATGAAAGGATGCAAGTTCATTAAGTCAAGCTGTT 1500
Db 2656 CTGCTTGAAGAGAAAGTCTATTCATGAAAGGATGCAAGTTCATTAAGTCAAGCTGTT 2715
Qy 1501 AAAATTCCAGGGGTGTGATGGGTTTCTTCCAGAAAGGCTTTAATTAAGGAAATATAG 1560
Db 2716 AAAATTCCAGGGGTGTGATGGGTTTCTTCCAGAAAGGCTTTAATTAAGGAAATATAG 2775
Qy 1561 GAAGCAGCTCAATTCCTAGGCGTTAATTCACGAAAGAGTCACTGAGTCTTTCTT 1620
Db 2776 GAAGCAGCTCAATTCCTAGGCGTTAATTCACGAAAGAGTCACTGAGTCTTTCTT 2835
Qy 1621 CATGTCTTGGGCAACTACTAGCCCTGTGTGACTTGGCTTAAGCAAGCGTGA 1680
Db 2836 CATGTCTTGGGCAACTACTAGCCCTGTGTGACTTGGCTTAAGCAAGCGTGA 2895
Qy 1681 AACCTTGAAGTCAAGAGACTGGGTTTCTTCTGAGTTCGCAATGGTGTGGCTGTGCGAC 1740
Db 2896 AACCTTGAAGTCAAGAGACTGGGTTTCTTCTGAGTTCGCAATGGTGTGGCTGTGCGAC 2955
Qy 1741 CGTGGCAAGTGTCTCTCTTCCCTGGGCATAGTCTTCTGTCTAATAAGCCCTTGA 1800
Db 2956 CGTGGCAAGTGTCTCTCTTCCCTGGGCATAGTCTTCTGTCTAATAAGCCCTTGA 3015
Qy 1801 GCTCTGTGTCTGTGAACAATTCCTGTGATCTTCTGTGAGGGGAGTGTGAAGGGG 1860
Db 3016 GCTCTGTGTCTGTGAACAATTCCTGTGATCTTCTGTGAGGGGAGTGTGAAGGGG 3075

Qy 1861 AAGAGGGCAGAGCTGGAGCCTGAGCCAAGGGGAGGTTGAGGGGAGACGAGAGCAGG 1920
Db 3076 AAGAGGGCAGAGCTGGAGCCTGAGCCAAGGGGAGGTTGAGGGGAGACGAGAGCAGG 3135
Qy 1921 CAGAACTGGTGTCTCATCACTGCTCACTGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1980
Db 3136 CAGAACTGGTGTCTCATCACTGCTCACTGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3195
Qy 1981 CATGCTTGAAGAAAGCTCAATGAACCAAGCCACATTTTCTTCCCTTAAGCATAGAC 2040
Db 3196 CATGCTTGAAGAAAGCTCAATGAACCAAGCCACATTTTCTTCCCTTAAGCATAGAC 3255
Qy 2041 AATGGATTTGGCATTACCAAAAAGATGAGAGCTTAACGTGTGTAGCTTTTGGCTTG 2100
Db 3256 AATGGATTTGGCATTACCAAAAAGATGAGAGCTTAACGTGTGTAGCTTTTGGCTTG 3315
Qy 2101 GCATTCAAAAAGCTGGGCGAGAGCAAGTGAATCCAGAGATGTGTAACTTTTCAAGCC 2160
Db 3316 GCATTCAAAAAGCTGGGCGAGAGCAAGTGAATCCAGAGATGTGTAACTTTTCAAGCC 3375
Qy 2161 TGAACAGACCCCAAGCCTCAGCAGTGAAGTCTGACAGACGAGTGAAGCTGACGCG 2220
Db 3376 TGAACAGACCCCAAGCCTCAGCAGTGAAGTCTGACAGACGAGTGAAGCTGACGCG 3435
Qy 2221 AGGGAGAGAGAAAGAAAGAGAGGATGTATGAGCAAGAAACAGATTCATTCAAG 2280
Db 3436 AGGGAGAGAGAAAGAAAGAGAGGATGTATGAGCAAGAAACAGATTCATTCAAG 3495
Qy 2281 GGCAGTGGGAATTGACACAGGGAATTATAGTCAAGTATCTGGGTTCTAGAGGCAAG 2340
Db 3496 GGCAGTGGGAATTGACACAGGGAATTATAGTCAAGTATCTGGGTTCTAGAGGCAAG 3555
Qy 2341 GCTATATGTGGGGGAAAAAAATCAAGTTCAGAGAGTGGGAGACTGATTTCTTAATAC 2400
Db 3556 GCTATATGTGGGGGAAAAAAATCAAGTTCAGAGAGTGGGAGACTGATTTCTTAATAC 3615
Qy 2401 TATATTTTCTTTTCAAGCTGAGTAATTCAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2460
Db 3616 TATATTTTCTTTTCAAGCTGAGTAATTCAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3675
Qy 2461 GTAAGTACTTAGTTCCTCTTATTAAGAACTCTTTTCTCTGTGAGTTAGCAGACA 2520
Db 3676 GTAAGTACTTAGTTCCTCTTATTAAGAACTCTTTTCTCTGTGAGTTAGCAGACA 3735
Qy 2521 AGGGCAATCCGTTTCTTTTAAACAGAAAGAAATCTTAAGATTAAGCCAAACAGT 2580
Db 3736 AGGGCAATCCGTTTCTTTTAAACAGAAAGAAATCTTAAGATTAAGCCAAACAGT 3795
Qy 2581 TCAAGCTTGAAGTCTTGTGACTATATGATGTGTTTTTGAAGAAATCATTTACGCAATGTT 2640
Db 3796 TCAAGCTTGAAGTCTTGTGACTATATGATGTGTTTTTGAAGAAATCATTTACGCAATGTT 3855
Qy 2641 TACTATCTGATTCAGAAATGAGACTAGTACCTTTGGTCAAGCTTAACAACCCAT 2700
Db 3856 TACTATCTGATTCAGAAATGAGACTAGTACCTTTGGTCAAGCTTAACAACCCAT 3915
Qy 2701 TTGTAATGTCTCAAGTTCAGGCTTAACGTGAGAACCAATCAATTAAGATAGATCTTT 2760
Db 3916 TTGTAATGTCTCAAGTTCAGGCTTAACGTGAGAACCAATCAATTAAGATAGATCTTT 3974
Qy 2761 AGAGCAACCTGTGTTTCTGAC-TCGTGAGGTGAGTGTGCGCAGGGCAGTTGGAATATTT 2819
Db 3975 AGAGCAACCTGTGTTTCTGAC-TCGTGAGGTGAGTGTGCGCAGGGCAGTTGGAATATTT 4034
Qy 2820 TACTTCAAAATATTAACACTGTGTTGTGTTAATTAACAATTAAGTGTCAAGGCAAT 2879
Db 4035 TACTTCAAAATATTAACACTGTGTTGTGTTAATTAACAATTAAGTGTCTAAGGCAAT 4094
Qy 2880 CATTAATTCAGAGCTTAAGATTAATCTTGTGACAGTTTGTGATATTAATTTGCTATTTGC 2939
Db 4095 CATTAATTCAGAGCTTAAGATTAATCTTGTGACAGTTTGTGATATTAATTTGCTATTTGC 4154

QY	2656	CCGATTTGTAATATGTCCTCAAGTTCAGGCTTAACTGACAGACCAATCAATTAAGAAATAGAA	2755
Db	480	CCCAATTTGTAATATGTCCTCAAGTTCAGGCTTAACTGACAGACCAATCAATTAAGAAATAGAA	539
QY	2756	TCCTTAGAGCAAACTGCTGTTCTCCACTCTGGAGGTGAGTCCGACAGGCACTTTGGAA	2815
Db	540	TCCTTAGAGCAAACTGCTGTTCTCCACTCTGGAGGTGAGTCCGACAGGCACTTTGGAA	599
QY	2816	TATTTACTTCACAGATATTTGACACTGTTGGTATTTAAACAATAAAGTTGCTCAAGG	2875
Db	600	TATTTACTTCACAGATATTTGACACTGTTGGTATTTAAACAATAAAGTTGCTCAAGG	659
QY	2876	CAATCAATATTTCAAGTGGCTTAAAGTTACTTTCAGACGTTTGGTATATTTATTTGGCTA	2935
Db	660	CAATCAATATTTCAAGTGGCTTAAAGTTACTTTCAGACGTTTGGTATATTTATTTGGCTA	719
QY	2936	TTGGCAATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAAGCAGGATTTATTA	2995
Db	720	TTGGCAATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAAGCAGGATTTATTA	779
QY	2996	CCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTCATTTTGTTTTATAC	3055
Db	780	CCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTCATTTTGTTTTATAC	839
QY	3056	ACCTTCTTACTPAATTTAAACATTTTATTCATTTGGAAATAGGCCATTAACCTCAAGGTG	3115
Db	840	ACCTTCTTACTPAATTTAAACATTTTATTCATTTGGAAATAGGCCATTAACCTCAAGGTG	899
QY	3116	TAAATPACAGTACCTGTGATTTTGTCAATTAACAATGAAATCAACAGACATTTTATATCTATA	3175
Db	900	TAAATPACAGTACCTGTGATTTTGTCAATTAACAATGAAATCAACAGACATTTTATATCTATA	959
QY	3176	TTACAGTTGTGACAGATACGTTGTGPAAGGAAATTTTATCTCAAAACCTACTTGGAAAT	3235
Db	960	TTACAGTTGTGACAGATACGTTGTGPAAGGAAATTTTATCTCAAAACCTACTTGGAAAT	1019
QY	3236	AGACCTCCTGCTGAGTCTGTGTTTTTAAACATATTAATAAACAATGTTTAAATTTGATAT	3295
Db	1020	AGACCTCCTGCTGAGTCTGTGTTTTTAAACATATTAATAAACAATGTTTAAATTTGATAT	1079
QY	3296	TTTGATATATCATATTTTCAATTAATCATTTGTTTCTTTGTAATCTATATTTATATTTTGA	3355
Db	1080	TTTGATATATCATATTTTCAATTAATCATTTGTTTCTTTGTAATCTATATTTATATTTTGA	1139
QY	3356	AAACATCTTTCGAGAGAGAGTCCCAAGATTCACCAATGAGGTCTTTGGATGACACACA	3415
Db	1140	AAACATCTTTCGAGAGAGTCCCAAGATTCACCAATGAGGTCTTTGGATGACACACA	1199
QY	3416	CACAGAGTAAAGACTGATTTAGAGGCTTAACTTGAACATTTGGTGCCTGAGATGCAAGCTG	3475
Db	1200	CACAGAGTAAAGACTGATTTAGAGGCTTAACTTGAACATTTGGTGCCTGAGATGCAAGCTG	1259
QY	3476	AAATTTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTGAGGGTGAGGGGGGAAA	3535
Db	1260	AAATTTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTGAGGGTGAGGGGGGAAA	1319
QY	3536	TCCTGCGCTTCTAATAGAAATGCTCTCCCTGGAAGCTGTGAGGGTGTCTCTTGTGTTCT	3595
Db	1320	TCCTGCGCTTCTAATAGAAATGCTCTCCCTGGAAGCTGTGAGGGTGTCTCTTGTGTTCT	1379
QY	3596	GGCTGAGCTGATTTTTTCTGTGCTCCCTGCTACGCTTAAAGGACCTGTGTTGGAAATCTCAG	3655
Db	1380	GGCTGAGCTGATTTTTTCTGTGCTCCCTGCTACGCTTAAAGGACCTGTGTTGGAAATCTCAG	1439
QY	3656	TTCTTAGAGATGTCCTTGGACAGAGTGCAGGTTCATATGATTTGACAGTGAATGAGAAA	3715
Db	1440	TTCTTAGAGATGTCCTTGGACAGAGTGCAGGTTCATATGATTTGACAGTGAATGAGAAA	1499
QY	3716	TATTAATCAGAAATATATATCTTGTGTAATATAGACACACAGTATCTCTGGTGTATAGTGTG	3775
Db	1500	TATTAATCAGAAATATATATCTTGTGTAATATAGACACACAGTATCTCTGGTGTATAGTGTG	1559

[illegible]

QY 3894 TCTGGAAGTTATTTTCTAAGATCTTGTCTGGACGCTGAAGGCAACCCCTGTGACA 3953
 DB 1680 TCTGGAAGTTATTTTCTAAGATCTTGTCTGGACGCTGAAGGCAACCCCTGTGACA 1739
 QY 3954 GCCCACCACCGCTCAGTGGCCACTCTGTCTTCCCTGAAAGGGCTGGCTCCCACT 4013
 DB 1740 GCCCACCACCGCTCAGTGGCCACTCTGTCTTCCCTGAAAGGGCTGGCTCCCACT 1799
 QY 4014 ATATATTAACCTCTCTGGAAGTCAAGCATGAGCAGCAAGGCAACCCATCCAGGCACTC 4073
 DB 1800 ATATATTAACCTCTCTGGAAGTGGGGATAGCCAGCAAGGCAACCCATCCAGGCACTC 1859
 QY 4074 TCAGCAGCAGAGCTTTCCAGAGAAAGCTCACCAAGCTCTGCAATGAGTTCTTCTG 4133
 DB 1860 TCAGCAGCAGAGCTTTCCAGAGAAAGCTCACCAAGCTCTGCAATGAGTTCTTCTG 1919
 QY 4134 TGCAGCTTGTGAGCTTTTGGGCTGTGATGCGCAGCTGTCCAGTGTCTTGTGCTG 4193
 DB 1920 TGCAGCTTGTGAGCTTTTGGGCTGTGATGCGCAGCTGTCCAGTGTCTTGTGCTG 1979
 QY 4194 CTTGTGTGGATGTGGGGGCCAGAGCAGCTCAGCTCAGGAAGGCCAATGACCAAGTGG 4253
 DB 1980 CTTGTGTGGATGTGGGGGCCAGAGCAGCTCAGCTCAGGAAGGCCAATGACCAAGTGG 2039
 QY 4254 CCGATGCAAGTATCCTTCACTGTGTGCTCCCAATGAATCCAGCTCCCAAGCAGAG 4313
 DB 2040 CCGATGCAAGTATCCTTCACTGTGTGCTCCCAATGAATCCAGCTCCCAAGCAGAG 2099
 QY 4314 CCAAGGCAATGTCAGTATCCATATTAACAGAGAGCAGACCAACGCTTAAGACT 4373
 DB 2100 CCAAGGCAATGTCAGTATCCATATTAACAGAGAGCAGACCAACGCTTAAGACT 2159
 QY 4374 GAGGCGCACCAAGCTCAGCTCAGCTCCCTGAGAGCTCTCCACCAATTGACTTTGGA 4433
 DB 2160 GAGGCGCACCAAGCTCAGCTCAGCTCCCTGAGAGCTCTCCACCAATTGACTTTGGA 2219
 QY 4434 CCAAGGCTGCCAGGCCCCAGAGAGCCAGAGAGGGCTGCAAGAGAGCTGGGCAACCTGAG 4493
 DB 2220 CCAAGGCTGCCAGGCCCCAGAGAGCCAGAGAGGGCTGCAAGAGAGCTGGGCAACCTGAG 2279
 QY 4494 GCGGAGCGGAGACCACTGTGAAACCCAAACAGAGAGTTGAGACTGTGCTTACAGCAACT 4553
 DB 2280 GCGGAGCGGAGACCACTGTGAAACCCAAACAGAGAGTTGAGACTGTGCTTACAGCAACT 2339
 QY 4554 CCTCCGAGACAAGTCACTGTCTGAGAGAGAGAAAGCACTAAGGCAAGAAATAGAA 4613
 DB 2340 CCTCCGAGACAAGTCACTGTCTGAGAGAGAGAAAGCACTAAGGCAAGAAATAGAA 2399
 QY 4614 TCTGCGCAGAGAGTTGAAAGCAGCAGAGAGTGAAGAGCTGAGAAAGGGCCAGTG 4673
 DB 2400 TCTGCGCAGAGAGTTGAAAGCAGCAGAGAGTGAAGAGCTGAGAAAGGGCCAGTG 2459
 QY 4674 TCCCGCAGACCCAGAGCACTGTGCTGGGCTGTGCCACAGGCTCCAGAGAAAGTAAAGATGC 4733
 DB 2460 TCCCGCAGACCCAGAGCACTGTGCTGGGCTGTGCCACAGGCTCCAGAGAAAGTAAAGATGC 2519
 QY 4734 AAGAGTGGGGGAGACTGAGTTGAGAGAGTATGCTGTGAGTGAACCTGTACAGAGCCG 4793
 DB 2520 AAGAGTGGGGGAGACTGAGTTGAGAGAGTATGCTGTGAGTGAACCTGTGTACAGAGCCG 2579
 QY 4794 TCCAGGCTTCCCTGCTGCTGCTTCTCTAGAGACTGCAAGCTAGACAGAGCAGATGA 4853
 DB 2580 TCCAGGCTTCCCTGCTGCTGCTTCTCTAGAGACTGCAAGCTAGACAGAGCAGATGA 2639
 QY 4854 ATTAAGGAAGAGCAGCAGATCACTTCAAGTATTAAGTATTAAGTCTGAGAGCTT 4913
 DB 2640 ATTAAGGAAGAGCAGCAGATCACTTCAAGTATTAAGTATTAAGTCTGAGAGCTT 2699
 QY 4914 CATTTAGATTAGTGTGAGAGTTCTTGTGCCCCCTCATGTGAGTTTACAGTCCATAG 4973
 DB 2700 CATTTAGATTAGTGTGAGAGTTCTTGTGCCCCCTCATGTGAGTTTACAGTCCATAG 2759
 QY 4974 CAAAAGGAAGAAATAAAAGACCGGAGTGAATGTGTGAT 5014

DB 2760 CAAAAGGAAGAAATAAAAGACCGGAGTGAATGTGTGAT 2800
 RESULT 11
 US-10-278-698-294
 ; Sequence 294, Application US/10278698
 ; Publication No. US20050037344A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Patharray GmbH
 ; APPLICANT: Stuhlmüller, Bruno
 ; APPLICANT: Haupt, Thomas
 ; TITLE OF INVENTION: Nucleic Acid Array
 ; FILE REFERENCE: 030027US
 ; CURRENT APPLICATION NUMBER: US/10/278, 698
 ; NUMBER OF SEQ ID NOS: 1050
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 294
 ; LENGTH: 2800
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-278-698-294
 Query Match 46.2%; Score 2773.4; DB 8; Length 2800;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2797; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
 QY 2216 ACGCGAGGGGAGAGAGAGAGAGAGAGATGATGATAGACAGAGAAAGACAGATTCA 2275
 DB 1 ACGCGAGGGGAGAGAGAGAG-AAAAGAGAGGATGATGATAGACAGAGAAAGACAGATTCA 59
 QY 2276 TCAAGGGCAGTGGGAATTAACAAGGATTTATGTCAGCTGATCTGGGTTCTAGAG 2335
 DB 60 TCAAGGGCAGTGGGAATTAACAAGGATTTATGTCAGCTGATCTGGGTTCTAGAG 119
 QY 2336 GCAGGGCTATATGTGGGGGGGAAAAAATCAGTTCAAGGGAGTGGGGAGACCTGATTCT 2395
 DB 120 GCAGGGCTATATGTGGGGGGGAAAAAATCAGTTCAAGGGAGTGGGGAGACCTGATTCT 179
 QY 2396 AATTAATATTTTCTTTCAAGCTGAGTAAATCTGAGCAAGTCAAGAGTAACTG 2455
 DB 180 AATTAATATTTTCTTTCAAGCTGAGTAAATCTGAGCAAGTCAAGAGTAACTG 239
 QY 2456 AGCGTGAAGATTACTTACTGTTCTCTTAATTAAGAACTTTTCTGTGAGATTAGA 2515
 DB 240 AGCGTGAAGATTACTTACTGTTCTCTTAATTAAGAACTTTTCTGTGAGATTAGA 299
 QY 2516 GCACAAAGGCATCCCGTTCTTTTACAGAGAAAGCACTCTTAAGATTAAGCCAA 2575
 DB 300 GCACAAAGGCATCCCGTTCTTTTACAGAGAAAGCACTCTTAAGATTAAGCCAA 359
 QY 2576 CAGATTCAAGCTTACGCTTGTGACTATATGATGTTTGTGAAAAATCATTTCAAGG 2635
 DB 360 CAGATTCAAGCTTACGCTTGTGACTATATGATGTTTGTGAAAAATCATTTCAAGG 419
 QY 2636 ATGTTTACTATGTGATTAAGAAATGAGACTAGTACCCTTTGGTCACTGTAAACAA 2695
 DB 420 ATGTTTACTATGTGATTAAGAAATGAGACTAGTACCCTTTGGTCACTGTAAACAA 479
 QY 2696 CCATTGTAATATGCTCAAGTTGAGGCTTAATGAGCAAAACCAATCAATTAAGATTA 2755
 DB 480 CCATTGTAATATGCTCAAGTTGAGGCTTAATGAGCAAAACCAATCAATTAAGATTA 539
 QY 2756 TCTTTAGCAAACTGTGTTTCTCCACTGAGAGTGAAGTGTGCCAGGCGAGTTGAAA 2815
 DB 540 TCTTTAGCAAACTGTGTTTCTCCACTGAGAGTGAAGTGTGCCAGGCGAGTTGAAA 599
 QY 2816 TATTTACTTCAAGATTAAGACAGTGTGTTGTTTAAACAATTAAGTGTCTAAAG 2875
 DB 600 TATTTACTTCAAGATTAAGACAGTGTGTTGTTTAAACAATTAAGTGTCTAAAG 659
 QY 2876 CAATCATATTTCAAGTGGCTTAAGATTACTTGAACAGTTTGGTATATTATTTGGCTA 2935

D6	660	CAATCATATTATTCAGAGGCTTAAAGTTACTCTGACGTTTGGTATTTATGCTAT	719
QY	2936	TTGCAATTGGCTTTTGTGTTTTCTCTTTGGGTTATTAATGTAAACAGGATTTAA	2995
D6	720	TTGCAATTGGCTTTTGTGTTTTCTCTTTGGGTTATTAATGTAAACAGGATTTAA	779
QY	2996	CTTACAGTCCGAAAGCCTGTGAATTGTGAATGAGAAAAATTACATTTTGTTTTACC	3055
D6	780	CTTACAGTCCGAAAGCCTGTGAATTGTGAATGAGAAAAATTACATTTTGTTTTACC	839
QY	3056	ACCTCTTAACTTAAATTTACATTTTATCCATGCGAATAGAGCATTAACCTCAAGTGG	3115
D6	840	ACCTCTTAACTTAAATTTACATTTTATCCATGCGAATAGAGCATTAACCTCAAGTGG	899
QY	3116	TAAATACAGTACCTGTGATTTTGTCAATTACCAATAGAAATCACAGACATTTTATCTATA	3175
D6	900	TAAATACAGTACCTGTGATTTTGTCAATTACCAATAGAAATCACAGACATTTTATCTATA	959
QY	3176	TTACAGTTGTTCAGATACGTTGTAGTGAATAATTTACTCAAAACTACTTTGAATTT	3235
D6	960	TTACAGTTGTTCAGATACGTTGTAGTGAATAATTTACTCAAAACTACTTTGAATTT	1019
QY	3236	AGACCTCCTGCTGGAATCTTGTTTTAAACATTTTAATTAACANAGTTTAAATTTTGATAT	3295
D6	1020	AGACCTCCTGCTGGAATCTTGTTTTAAACATTTTAATTAACANAGTTTAAATTTTGATAT	1079
QY	3296	TTTGATATTCATATTTCATATTCATTTTGTCTCTTGTGAATCTAATTTTATATTTTGA	3355
D6	1080	TTTGATATTCATATTTCATATTCATTTTGTCTCTTGTGAATCTAATTTTATATTTTGA	1139
QY	3356	AAACATCTTCTGAGAGAAGTTCCCGACATTTTCCCAATGAGGTTCTTGGCATCACA	3415
D6	1140	AAACATCTTCTGAGAGAAGTTCCCGACATTTTCCCAATGAGGTTCTTGGCATCACA	1199
QY	3416	CACAGATTAAGAACTGATTTTAGAGGCTAACATTGACATTTGGTGCCTGAGATGCAAGCTG	3475
D6	1200	CACAGATTAAGAACTGATTTTAGAGGCTAACATTGACATTTGGTGCCTGAGATGCAAGCTG	1259
QY	3476	AAATTAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTGAGGGGTGAGGGGGAAA	3535
D6	1260	AAATTAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTGAGGGGTGAGGGGGAAA	1319
QY	3536	TCGCGCGTCTTAATAGAAATGCTCTCCCTGAGAGCTGTGTAGGGTGTCTCTTGTGTTCT	3595
D6	1320	TCGCGCGTCTTAATAGAAATGCTCTCCCTGAGAGCTGTGTAGGGTGTCTCTTGTGTTCT	1379
QY	3596	GGCTGGCTGTTATTTTCTCTGTCTCCCTGTACGTTTAAAGACTTGTTTGATCTCCAG	3655
D6	1380	GGCTGGCTGTTATTTTCTCTGTCTCCCTGTACGTTTAAAGACTTGTTTGATCTCCAG	1439
QY	3656	TTCCTAGAATAGTGTGTCGACAGTGCAGGTTCTCAAGAGTTTGCACAGTGAATGGAAA	3715
D6	1440	TTCCTAGAATAGTGTGTCGACAGTGCAGGTTCTCAAGAGTTTGCACAGTGAATGGAAA	1499
QY	3716	TATAAATAGAAATATATCTCTGTGTGAATCAGCACACAGTAGTCTGTGTAAAGTGTG	3775
D6	1500	TATAAATAGAAATATATCTCTGTGTGAATCAGCACACAGTAGTCTGTGTAAAGTGTG	1559
QY	3776	TGTAC--GT	3833
D6	1560	TGTACGT	1619
QY	3834	TATTGGGGATATGGGTCATAAATGGAGATGTTCTTTTAAAGAAATCTCCAAACAGACT	3893
D6	1620	TATTGGGGATATGGGTCATAAATGGAGATGTTCTTTTAAAGAAATCTCCAAACAGACT	1679
QY	3894	TCGTGAAGGTATTTTCTTAAGATCTTGCTGTGACGTGAAGGCAACCCCTGTGCACA	3953
D6	1680	TCGTGAAGGTATTTTCTTAAGATCTTGCTGTGACGTGAAGGCAACCCCTGTGCACA	1739
QY	3954	GCCCAACCCAGCTCAGTGGCACCTGTCTTCCCATGAGAGGCTGTGCTCCCAAGT	4013

Db	1740	DOCCACCACGAGCTCAGCGTGGCACCTGTGTCTTCCCCCATAAAGGGCTGGCTCCCAAGT	1799
Qy	4014	ATATATAAACTCTCTGAGAGCTCAGGCAATGAGCCAGCAAGGCCACCCATTCAGAGCACTTC	4073
Db	1800	ATATATAAACTCTCTGAGAGCTCAGGCAATGAGCCAGCAAGGCCACCCATTCAGAGCACTTC	1859
Qy	4074	TCAGACAGCAGAGAGCTTTCAGAGGAAAGCTCACCAAGGCTCTGCATATAGAGTTCCTTCG	4133
Db	1860	TCAGACAGCAGAGAGCTTTCAGAGGAAAGCTCACCAAGGCTCTGCATATAGAGTTCCTTCG	1919
Qy	4134	TGCAAGTGTCTGCAAGCTTGTGGGCTGAGATGCGCAAGTGTCCAGCTGTCTCTTCTGGGCTTG	4193
Db	1920	TGCAAGTGTCTGCAAGCTTGTGGGCTGAGATGCGCAAGTGTCCAGCTGTCTCTTCTGGGCTTG	1979
Qy	4194	CCTGCTGTGGATGTGGGGGCGCAGACAGCTCAGCTCAGAAAGGCCAATGACCAAGTGG	4253
Db	1980	CCTGCTGTGGATGTGGGGGCGCAGACAGCTCAGCTCAGAAAGGCCAATGACCAAGTGG	2039
Qy	4254	CCGATGCGCAATATACCTTCAGTGTGGCCAGTCCCAATGAAATCAGCTGCGCCAGAGCAGAG	4313
Db	2040	CCGATGCGCAATATACCTTCAGTGTGGCCAGTCCCAATGAAATCAGCTGCGCCAGAGCAGAG	2099
Qy	4314	CCAGGCGCATGTCAAGTCATCATTAATTACAGAGAGCAGACAGCAACCAAGCTTAAAGCT	4373
Db	2100	CCAGGCGCATGTCAAGTCATCATTAATTACAGAGAGCAGACAGCAACCAAGCTTAAAGCT	2159
Qy	4374	GGAGGCGCACAAAGCTCGAGCTCAGCTCTGAGAGAGCTCTTCACCAATTTGACTTTGGA	4433
Db	2160	GGAGGCGCACAAAGCTCGAGCTCAGCTCTGAGAGAGAGCTCTTCACCAATTTGACTTTGGA	2219
Qy	4434	CGAGGCTGCGAGGCCCCCAGAGAACCCAGAGAGGGGCTGCGAGAGGAGACTGGGGACCCCTGAG	4493
Db	2220	CGAGGCTGCGAGGCCCCCAGAGAACCCAGAGAGGGGCTGCGAGAGGAGACTGGGGACCCCTGAG	2279
Qy	4494	GGGGAGGCGGAGCCAGAGCTGGAATCCAAACCAAGAGAGTTGAGACTGCTCAACAGCAACT	4553
Db	2280	GGGGAGGCGGAGCCAGAGCTGGAATCCAAACCAAGAGAGTTGAGACTGCTCAACAGCAACT	2339
Qy	4554	CCTCCGAGACAAAGTCAGTTCTGAGAGAGAGAGAAAGCGACTAAGGCCAAGAAAATGAGAA	4613
Db	2340	CCTCCGAGACAAAGTCAGTTCTGAGAGAGAGAGAAAGCGACTAAGGCCAAGAAAATGAGAA	2399
Qy	4614	TTTGAGCCAGAGAGTTTGAAGACAGACAGCCAGAGAGTTAGCAAGGCTGAGAAAGGGGCCAGTG	4673
Db	2400	TTTGAGCCAGAGAGTTTGAAGACAGACAGCCAGAGAGTTAGCAAGGCTGAGAAAGGGGCCAGTG	2459
Qy	4674	TCCCCAGACCCGAGACACTGCTCGGGCTGAGCCAGCAGAGGCTCAGAGAAAGTAAAGATGC	4733
Db	2460	TCCCCAGACCCGAGACACTGCTCGGGCTGAGCCAGCAGAGGCTCAGAGAAAGTAAAGATGC	2519
Qy	4734	AAGAGTGGGGGAGCTCTGAGTTGAGCAGAGTGAATATGCTCGTAGTGAACCTCTACAGGCGC	4793
Db	2520	AAGAGTGGGGGAGCTCTGAGTTGAGCAGAGTGAATATGCTCGTAGTGAACCTCTACAGGCGC	2579
Qy	4794	TTCAGGCTTCCTGCTGCTGCTCTTCTCTAGAGACTGACACAGCTTACAGTGAATGAGATGA	4853
Db	2580	TTCAGGCTTCCTGCTGCTGCTCTTCTCTAGAGACTGACACAGCTTACAGTGAATGAGATGA	2639
Qy	4854	ATTAAAGGAAAGCAGAGCGATACACCTCAAGTATTTACTAGTAATTTAGCTCTGAGAGCTT	4913
Db	2640	ATTAAAGGAAAGCAGAGCGATACACCTCAAGTATTTACTAGTAATTTAGCTCTGAGAGCTT	2699
Qy	4914	CATTATGATTAGTGTTCAGAGTTCTTGTGCCCCCTCATATGCTCAGTTTTCACAGTCCATAG	4973
Db	2700	CATTATGATTAGTGTTCAGAGTTCTTGTGCCCCCTCATATGCTCAGTTTTCACAGTCCATAG	2759
Qy	4974	CAAAAGAGAAATTAAGAGACCGGGTGAATGTGTCTGCAT	5014
Db	2760	CAAAAGAGAAATTAAGAGACCGGGTGAATGTGTCTGCAT	2800

Db	1740	DOCCACCACGAGCTCAGCGTGGCACCTGTGTCTTCCCCCATAAAGGGCTGGCTCCCAAGT	1799
Qy	4014	ATATATAAACTCTCTGAGAGCTCAGGCAATGAGCCAGCAAGGCCACCCATTCAGAGCACTTC	4073
Db	1800	ATATATAAACTCTCTGAGAGCTCAGGCAATGAGCCAGCAAGGCCACCCATTCAGAGCACTTC	1859
Qy	4074	TCAGACAGCAGAGAGCTTTCAGAGGAAAGCTCACCAAGGCTCTGCAATAGAGGTTCTTCTG	4133
Db	1860	TCAGACAGCAGAGAGCTTTCAGAGGAAAGCTCACCAAGGCTCTGCAATAGAGGTTCTTCTG	1919
Qy	4134	TGCAAGTGTCTGCAAGCTTGTGGGCTGAGATGCGCAAGTGTCCAGCTGTCTCTTCTGGGCTTG	4193
Db	1920	TGCAAGTGTCTGCAAGCTTGTGGGCTGAGATGCGCAAGTGTCCAGCTGTCTCTTCTGGGCTTG	1979
Qy	4194	CCTGGTGTGGATGTGGGGGCCAGAGCAGCTCAGCTCAGAGAAAGGCCAATGACCAAGTGG	4253
Db	1980	CCTGGTGTGGATGTGGGGGCCAGAGCAGCTCAGCTCAGAGAAAGGCCAATGACCAAGTGG	2039
Qy	4254	CCGATGCGCAATATACCTTCAAGTGTGGCCAGTCCCAATGAAATCAGCTGCGCCAGAGCAG	4313
Db	2040	CCGATGCGCAATATACCTTCAAGTGTGGCCAGTCCCAATGAAATCAGCTGCGCCAGAGCAG	2099
Qy	4314	CCAGGCCATGTCAATCATCATTAATTACAGAGAGCAGCAGAGCACCAGCTTGAACCT	4373
Db	2100	CCAGGCCATGTCAATCATCATTAATTACAGAGAGCAGCAGAGCACCAGCTTGAACCT	2159
Qy	4374	GGAGGCCACCAAAAGCTCGACTCAGCTCCCTGAGAGAGCTCTTCACCAATTTGACTTTGA	4433
Db	2160	GGAGGCCACCAAAAGCTCGACTCAGCTCCCTGAGAGAGAGCTCTTCACCAATTTGACTTTGA	2219
Qy	4434	CCAGGCTGCGAGAGCCCGCAGAGAACCCAGAGAGGGGCTGCGAGAGGAGCCTGGGACCCCTGAG	4493
Db	2220	CCAGGCTGCGAGAGCCCGCAGAGAACCCAGAGAGGGGCTGCGAGAGGAGCCTGGGACCCCTGAG	2279
Qy	4494	GGGGAGGCGGAGCCAGCTGGAATCCCAACCAAGAGGTTGAGACTGCTCAACAGCAACT	4553
Db	2280	GGGGAGGCGGAGCCAGCTGGAATCCCAACCAAGAGGTTGAGACTGCTCAACAGCAACT	2339
Qy	4554	CCTCCGAGACCAAGTCAGTTCTGAGAGGAGAGAGAAAGCGACTAAGCCAAAGAAATGAGAA	4613
Db	2340	CCTCCGAGACCAAGTCAGTTCTGAGAGGAGAGAGAGAAAGCGACTAAGCCAAAGAAATGAGAA	2399
Qy	4614	TCTGGCCAGAGAGTTTGAAGACAGACGCCAGAGAGTTAGCAAGGCTGAGAAAGGGGCCAGTG	4673
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Qy	4674	TCCCCAGACCCGAGACACTGCTCGGGCTGAGCCAGCAGAGGCTCCAGAGAAAGTAAAGATGC	4733
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Db	2520	AGAGTGGGGGAGCTCTGAGTTGAGCAGAGTATATGCTCGTAGTGACTTGCTACAGGCGC	2579
Qy	4794	TTCAGGCTTCCTGCTGCTGCTTTCTCTAGAGACTGACACAGCTAGCACAAGCAGATGA	4853
Db	2580	TTCAGGCTTCCTGCTGCTGCTTTCTCTAGAGACTGACACAGCTAGCACAAGCAGATGA	2639
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Db	2640	ATTTAAGGAAAGCAGAGCGATACACCTCAAGTATTTACTAGTAATTTAGCTCTGAGAGCTT	2699
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Db	2700	CATTATGATTAGTGTTCAGAGTTCTTGTGCCCTCCATCTCAGTTTTCACAGTCCATAG	2759
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OY 4134 TGCAGGTTGCTGACAGCTTTGGGCTGAGATGCGACGCTGTGCACTGCTTCTGGCCTG 4193
DB 1920 TGCAGGTTGCTGACAGCTTTGGGCTGAGATGCGACGCTGTGCACTGCTTCTGGCCTG 1979
OY 4194 CTTGTGTGGATGTGGGGGCGACAGACGCTCAGCTCAGAGAAAGCAATGACCGAGTGG 4253
DB 1980 CTTGTGTGGATGTGGGGGCGACAGACGCTCAGCTCAGAGAAAGCAATGACCGAGTGG 2039
OY 4254 CCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGATCCAGCTGCCAGAGCAGAG 4313
DB 2040 CCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGATCCAGCTGCCAGAGCAGAG 2099
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DB 2100 CCAAGGCATGTGATCATTCATTAACAGAGAGACAGACACCCAAACGTTAGACTT 2159
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OY 4434 CCAAGGCTCCAGAGCCCGACAGAGACCCAGAGAGGCTGACAGAGGAGCTGGCACTTGAG 4493
DB 2220 CCAAGGCTCCAGAGCCCGACAGAGACCCAGAGAGGCTGACAGAGGAGCTGGCACTTGAG 2279
OY 4494 GCGGGAGCGGGACCAAGCTGGAAAACCCAAACAGAGAGTTGAGACTGCTTACAGCAACT 4553
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DB 2760 CAAAAGAGAGAAATTAAGAGACCGAGTGAAGTGTCTGCAT 2800

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RESULT 13
US-10-803-557-10
; Sequence 10, Application US/10803557
; Publication No. US20050095609A1
; GENERAL INFORMATION:
; APPLICANT: HUNAG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401

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; CURRENT APPLICATION NUMBER: US/10/803,557
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: US/10/017,870
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-557-10

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Query Match 46.2%; Score 2773.4; DB 9; Length 2800;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2797; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

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OY 2336 GCAAGGCTATATTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2395
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OY 2456 AGGCTGTAAGTATCTTAAGTTCTCTTATTAAGAGAACTCTTTTCTCTGTGAGTTAGCA 2515
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DB 300 GCAAGAGGCAATCCCGTTTCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
OY 2576 CAGATTCAAGCTTGAAGTTTCTGCTGATATATGATTTGTTTGAAGAAATCAATTCAGAG 2635
DB 360 CAGATTCAAGCTTGAAGTTTCTGCTGATATATGATTTGTTTGAAGAAATCAATTCAGAG 419
OY 2636 ATGTTTACTATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2695
DB 420 ATGTTTACTATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
OY 2696 CCCATTGTAAATGTCTCAAGTTCAAGGCTTAACTGACAGAACCAATCAATTAAGATGA 2755
DB 480 CCCATTGTAAATGTCTCAAGTTCAAGGCTTAACTGACAGAACCAATCAATTAAGATGA 2800
OY 2756 TCTTTAGAGCAAACTGTGTTTCTCCACTGAGAGTGTGCTGCAAGGAGTTTGGAAA 2815
DB 540 TCTTTAGAGCAAACTGTGTTTCTCCACTGAGAGTGTGCTGCAAGGAGTTTGGAAA 599
OY 2816 TATTTACTTCAAGATATGACACTGTTGTTGTTTAAACAATTAAGTGTCTCAAGAG 2875
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OY 2876 CAATCATTTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGTGATATTTATGGCTA 2935
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OY 2996 CCTACAGTCCAGAAAGCCGTTGAATTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3055
DB 780 CCTACAGTCCAGAAAGCCGTTGAATTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
OY 3056 ACCTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3115

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OY	4319	CCATGTCAGTCATCCATACTTACAGAGAGACAGACGACCCCAACGCTTAAAGCTTGAGG	4378
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OY	4379	CCACCAAAAGCTGAGCTCAGCTCCCTGAGAGCTTCCTCCACCAATTGACCTTGAGCCAGG	4438
Db	721	CCACCAAAAGCTGAGCTCAGCTCCCTGAGAGCTTCCTCCACCAATTGACCTTGAGCCAGG	780
OY	4439	CTGCCAAGGCCCCAGAGAGCCCAAGAGGCGCTGCAAGAGGAGCTGGGCACTCGAGGCGGG	4498
Db	781	CTGCCAAGGCCCCAGAGAGCCCAAGAGGCGCTGCAAGAGGAGCTGGGCACTCGAGGCGGG	840
OY	4499	AGCGGACCAAGCTGGAACCCCAACCAAGAGTTGAGAGCTGCTACAGCAACTCTCTCC	4558
Db	841	AGCGGACCAAGCTGGAACCCCAACCAAGAGTTGAGAGCTGCTACAGCAACTCTCTCC	900
OY	4559	GAGACAAGTCAGTTCTGAGAGAGAGAGAAAGCACTAAGGCAAGAAAAATGAAATCTGG	4618
Db	901	GAGACAAGTCAGTTCTGAGAGAGAGAGAGAAAGCACTAAGGCAAGAAAAATGAAATCTGG	960
OY	4619	CCAGAGGTTGGAAGCAGCAGCCAGAGGTAGCAAGGCTGAGAAAGGGCCAGTGTCCCC	4678
Db	961	CCAGAGGTTGGAAGCAGCAGCCAGAGGTAGCAAGGCTGAGAAAGGGCCAGTGTCCCC	1020
OY	4679	AGACCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGAGAGGTAAAGATGACAGAGT	4738
Db	1021	AGACCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGAGAGGTAAAGATGACAGAGT	1080
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Db	1081	GGGGGG 1086	

Search completed: March 24, 2006, 07:53:22
 Job time : 4280 secs

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RESULT 2
US-09-925-065A-917000/c
Sequence 917000, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 917000
LENGTH: 630
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-917000

Query Match 10.5%; Score 629.6; DB 6; Length 630;
Best Local Similarity 99.8%; Pred. No. 0.0001;
Matches 629; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      210 CTCAATCTCTCATTTTCAAGGCTAAGTTACCATTTTATTCACCAATGCTTTTGTGTAAGCT 151
Qy      550 CACATCTCTCATTTTCAAGGCTAAGTTACCATTTTATTCACCAATGCTTTTGTGTAAGCT 609
Db      150 CACATCTCTCATTTTCAAGGCTAAGTTACCATTTTATTCACCAATGCTTTTGTGTAAGCT 91
Qy      610 GTGATATGAGGAGAGGAGGATATCCCAAGAGACTCTTGAAGCCCCCGCAGAGGTTTCT 669
Db      90 GTGATATGAGGAGAGGAGGATATCCCAAGAGACTCTTGAAGCCCCCGCAGAGGTTTCT 31
Qy      670 CTCACAGCTGGGGGAGCCCTGCAAGCACC CG 699
Db      30 CTCACAGCTGGGGGAGCCCTGCAAGCACC CG 1

```

RESULT 3
US-09-925-065A-346049
Sequence 346049, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 346049
LENGTH: 571
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-346049

Query Match 9.5%; Score 570.6; DB 6; Length 571;
Best Local Similarity 99.8%; Pred. No. 0.0011;
Matches 570; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2672 CCTTGGTGCAGCTGTAACAAACACCCATTGTAATGCTCAAGTTCAGGCTTAACCTGC 2731
 DB 1 CCTTGGTGCAGCTGTAACAAACACCCATTGTAATGCTCAAGTTCAGGCTTAACCTGC 60
 QY 2732 AGAACCAATGAATTAAGTAATGTAATCTTTAGAGAACTGTGTTCTCCACTGCGAGGT 2791
 DB 61 AGAACCAATGAATTAAGTAATGTAATCTTTAGAGAACTGTGTTCTCCACTGCGAGGT 120
 QY 2792 GAGCTGCGCAGGCGAGTTGGAAATATTTACTTCACAGATTTGACACTGTGTGGTAT 2851
 DB 121 GAGCTGCGCAGGCGAGTTGGAAATATTTACTTCACAGATTTGACACTGTGTGGTAT 180
 QY 2852 TAAACAATTAAGTGTCTCAAGGCAATCATTTATTCAGTGGCTTAAAGTTACTTGA 2911
 DB 181 TAAACAATTAAGTGTCTCAAGGCAATCATTTATTCAGTGGCTTAAAGTTACTTCTGA 240
 QY 2912 CAGTTTGTATTTATTTATTTGGCTATTTGGCTATTTGCTTTTCTTTTCTTTGGGTTTA 2971
 DB 241 CAGTTTGTATTTATTTATTTGGCTATTTGGCTATTTGCTTTTCTTTTCTTTGGGTTTA 300
 QY 2972 TTAATGTAAAGCAGGAGTTATTTAACTTACCTACAGTCCAGAAAGCTGTGAATTTGAATGAGA 3031
 DB 301 TTAATGTAAAGCAGGAGTTATTTAACTTACCTACAGTCCAGAAAGCTGTGAATTTGAATGAGA 360
 QY 3032 AAAAATTAATTTTGTGTTTACCACTTCTTAACTTAATTTAACTTTTATTCATTTGCG 3091
 DB 361 AAAAATTAATTTTGTGTTTACCACTTCTTAACTTAATTTAACTTTTATTCATTTGCG 420
 QY 3092 AATAGAGCCATAAATCTCAAGTGTATTAACAGTACCTGTGATTTTGTCTTACCAATAG 3151
 DB 421 AATAGAGCCATAAATCTCAAGTGTATTAACAGTACCTGTGATTTTGTCTTACCAATAG 480
 QY 3152 AATACAGACATTTTATCTATTTATTAAGTGTGAGATGAGTGGTAAAGTAATTT 3211
 DB 481 AATACAGACATTTTATCTATTTATTAAGTGTGAGATGAGTGGTAAAGTAATTT 540
 QY 3212 TATACTCAAAAATCTTTGAAATTAAGACTC 3242
 DB 541 TATACTCAAAAATCTTTGAAATTAAGACTC 571

RESULT 4
 US-11-136-527-717
 ; Sequence 717, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Nouns, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-04100 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/54,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 717
 ; LENGTH: 16525
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-11-136-527-717

Query Match 9.4%; Score 566.2; DB 12; Length 16525;
 Best Local Similarity 62.6%; Pred. No. 0.0001;
 Matches 1201; Conservative 0; Mismatches 608; Indels 110; Gaps 16;
 QY 3164 TTTTATTAATTAATTAAGTGTGAGATAGCTGTGTAAGTAATTTATTAATCTCAAAAC 3223
 DB 5339 TTTATTCCTGCTGTATGAGCTGATGAGCTTCCATGAAA---TGTGTATGTAATCTCAAGG 5395
 QY 3224 TACTTTGAATTAAGACTCTGTGATCTGTGTTTAACTATTAATTAATTAATCAATGTTTA 3283
 DB 5396 TCTTTTAAATTAAGACTTATGATGCTGATCTTTATTAATTAATTAATTAATTCAGGCTTTAA 5455

QY 3284 AATTTGATTAATTTGATATCATATTTGATTAATTTGTTTCTTTGTAATCTAATTT 3343
 DB 5456 TATTTTCAATGCTTAAATTAATGAGCTTTCTTTTATTAATCTT-----TACAT 5503
 QY 3344 TTAATTAATTTGAAACATCTTTCTGAGAAAGTTCCAGATTTTCAATGAGTTCCT 3403
 DB 5504 TTAATGATTTGAGCTTTCTTTTCAAGATG--GACGCAAGATTTTCAAGTATACCTTTTG 5562
 QY 3404 GGCATGCAACACAGAGTAAGAACTGATTTAGAGCTTAACATTAACATTTGCTGCTGA 3463
 DB 5563 GGCACACCTCATATTAATTAATGAGCTTCAAG-----CATGCAAGAGCTTCTTGA 5611
 QY 3464 GATGCAAGCTGAAATTAAGAAAGTTCTCCAAAGATACAGTGTGTTTAAAGCTAGGG 3523
 DB 5612 GACACAGGCTGATGACAGAGATTTTCTTAAGACACACATGATTAATTTCAACCTTA 5671
 QY 3524 TGAAGGGGGAATCTGCGCTTCTATAGGAATGCTCTCCCTGAGAGCTGTAGGGTCTG 3583
 DB 5672 GGGCGGCATCATGTTCTCACCCCT-----TGTGAGAGCTTGAAGCTGTG 5719
 QY 3584 TCTTGTGTTCTGCTGCTGCTGTTATTTTCTGTCTGCTGCTAAGCTTTAAAGACTGT 3643
 DB 5720 GCACTGCGCTCTTCCCTGCGGCTCTTCTGTCT--CGGCTACAGGCGATGTCTGCTATGT 5778
 QY 3644 TTGAATCTGAGTCTTACATAGTCCGAGAGCTGAGAGTGTCTCATAGACTTTCAG 3703
 DB 5779 CTGTCTCTTATGCTTTACAGAGTACGTGTCAGAGAGGAGTCTTA----- 5826
 QY 3704 AGTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3762
 DB 5827 -----TGAACACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5879
 QY 3763 TGTGTAATGTGTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3822
 DB 5880 CAGAGAGGTGGCATACGCGACATGT-----ACAAACAGGCTGAAAC 5924
 QY 3823 ATAGGAATTAATTTGGGGTATGGGATGAATTTGGGATGTTTCTTTTAAAGAAAT 3882
 DB 5925 TTAGGGCTTATTAATGAGATGTGG--GTACATGCCGGGAGCTTAAATTAATTAATTC 5981
 QY 3883 CCAAACAGACTTCTGAAAGTATTTTCTAAGATCTTGTGCTGAGCGTGAAGCAACC 3942
 DB 5982 AAAATAGCTCTGAGGCTTTATTTTAAATCTTGTGCTGAGTGAATCCATTC 6041
 QY 3943 CCTGTGAC-----AGCCCAACAGCTTCAAGTGGCCACTGTGTCTTCCCAT 3994
 DB 6042 TCTATATCCCCCATGAGTGTGTCAAACCAAGCTTCAATGATCATCTTCCCTCCAC 6101
 QY 3995 GAAAGGCTGCTCCCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4054
 DB 6102 AAGAGGCTGCTCCCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4161
 QY 4055 CCACCATTCAGGCACTCTCTGACACAGAGCTTTTCAAGAGAGCTTCAAGAGCT 4114
 DB 6162 CCACCATTCAGGCACT-----TGCAGAGAGCTTCTAAGAGAGCTTCAAGAGCT 6216
 QY 4115 CTGCAATAGGTTCTTCTGTGACAGTGTGAGCTTGTGGCTGAGATGCCAGTGTCC 4174
 DB 6217 TCAATACCATGCTCTCTGTGACAGCTGTGAGCTGTGGCTTCCAAAGATGCCAGTGTCC 6276
 QY 4175 AGCTGCTGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4234
 DB 6277 AGCTGCTGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6336
 QY 4235 AGGCCAATGACAGAGTGGCGATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4294
 DB 6337 AGGCCAATGACAGAGTGGCGATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6396
 QY 4295 CCAAGTCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4354
 DB 6397 CTAAGTCTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6456

OY	4355	GCACCCAAACGCTTGA	CCCTGGAGGCGACCAAAAGCTGCACTGACCTCC	TGAGAGGCTCC	441.4
Db	6457	GCATCCAGCAATGCAG	ACTTAAGTCCACCAAGGCCGGGTCAAGATCCCTGGAGATCTCC		651.6
OY	4415	TCACAACCAATTGAC	CTTTGGACCAAGCTGCGCAAGGCCCAAGAGACCCAGAGAGGGGACTGCAGA		447.4
Db	6517	TCACACCAATGACCT	CAGCGGAGTTATCTGGGACCCAGAGAGGTCCAGAGGGGGCTTACAAG		657.6
OY	4475	GGGAGCTGGGCA	CCCTGAGGCGGGAGCGGGACACGCTGAGAAACCAACCAAGAGGTTGG		453.3
Db	6577	GCACGCTGGGTC	CCCTGAGAGAGGCGGGACCACTGAGACCCAAACAGGGATCTGG		663.3
OY	4535	AGACTGCTCAGCA	CACTCTCTCCAGACAAGTCACTTCTGAGGAGAGAGAAAGCAGC		459.9
Db	6637	AGGTAGCTTATPACA	ATCTCTGAGAGACAATTCAGCTTTGGAGAGAGAAAGAGCAGC		669.9
OY	4585	TAAGGCACAAATATG	AGATCTGGCCAGAGGTTGGAAAACGACGACCCAGAGGTTAGCA		465.5
Db	6697	TGGAACAAAGAGAT	TTAAGATTTGGCCAGAGGCTTGAAGGACGACGACGAGGTTAGCA		675.5
OY	4655	GGCTGAGAAAGGGG	CCAGTGTCCCGACGCCGAGACACTGCTCGGGCTGACCAAGGCT		471.1
Db	6757	GGCTGAGAGAGG	CCAGTGTCCCGACGCCCTCTGAGACATGTTGGCCAGGCT		681.1
OY	4715	CCAGAGAAAGTAA	GATGCAAGTGGGGAGCTTGAG-TTCAGAGGTGATATGACTCG		477.7
Db	6817	CCAGGGAAGTTA	GAGATCGGGGGTGGAGGGGCTGACTGACCCGGAAGGTAGCAATTTGCG		687.7
OY	4774	TAGTGA	CCCTGACAGGCGCTCCAGAGCTCCCTGCGCTGCCCTTCT-----CTAAGAGA		482.2
Db	6877	GGGTACCTATTA	CCAGACTCCCAAGCTCTCTCTTTGTTGTCTTTCTCTCACTAATA		693.3
OY	4828	CTGCACAGCTAGCA	CAGAAGCATGTAATTAAGAAAGCACAGCATCACTTCAAGTAT		488.8
Db	6937	CTGAAGTCCAGTAT	GACGTATTCATTAAGAAAGCAAGCAAACTTTTCATGTT		699.9
OY	4888	ACTAGTAA	TTTAGCTTCGAGAGCTTCATTTAGATTAAGTGTTCAGAGTCTTTGTGCCCC		494.4
Db	6997	TCCTCAAGTTGACT	-----CGTTGTTTAGGCGAGTGATCTGAAGCTCTTGTCCTCA		704.4
OY	4948	TCATATGCA	TTTTTTCACAGTCCATAGCAAAAGAGAAATPAAAGACCGGGTGAGATGTC		500.0
Db	7049	GTCAATGACAAAT	TGATCAACAGCACAGCCAAATGAGAAACAGGGGGCCAAAGTAGAGG--		710.0
OY	5008	TCTGCATATGAG	CAGTGAAGAGTTGCAATGTCCCTTTGAAAACTATCCCTTTTGG		506.6
Db	7107	--TGACATGTGG	AATAGAAAATGCGCTGCTGCTTGGGTCAATTTTCAAGCTTGG		716.3

```

/ RESULT 5
/ US-09-925-065A-346051
/ Sequence 346051, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 346051

```

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; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-346051

```

Query Match	9.0%	Score 543	DB 6	Length 545
Best Local Similarity	99.6%	Pred. No. 0.0034		
Matches 543; Conservative	1	Mismatches	1	Indels 0; Gaps 0

[illegible]

```

RESULT 6
US-09-925-065A-346050
; Sequence 346050, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FaastSQ for Windows Version 4.0

```


OTHER INFORMATION: n = A, T, C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13364

LENGTH: 1744

9463 CTGGGATTAAGGCATTAGCCACTGCGCCCCGACAAACAATTCAAATCTTAACAAACAAAA 9404

Qy 360 CTTGATGTTTACTAAACCAAGGAAACAGAAAGCTGTGATTAATTCAG 415
 Db 9403 TAATATATATATAATTAAGAAAGAAAAAACAATAATATAGCATATTACGG 9348

RESULT 14
 US-10-995-561-13274

; Sequence 13274, Application US/10995561
 ; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 13274

; LENGTH: 415117

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(415117)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13274

Query Match 3.1%; Score 183.4; DB 8; Length 415117;

Best Local Similarity 76.5%; Pred. No. 36;

Matches 241; Conservative 0; Mismatches 66; Indels 8; Gaps 1;

Qy 65 AGCGTGAAGGCTGTGTCTTACCTACCTGATGCTCTACCGAGCTGACGCAACC 124

Db 60473 AGAGCTTGTCTGTACCCACGCTGTAGTGAATGCGCAATCTCACTGCAACC 60532

Qy 125 TCTGCTCCCAAGTTCAGCAATTCCTGCTCAGCTCCCGAGCTGAGCAATGAG 184

Db 60533 TCCGCTCCCAAGTTCAGCAATTCCTGCTCAGCTCCCGAGCTGAGCAATGAG 60552

Qy 185 GCG-----CAGCCCGGCTAATTTTGTATGTAAGTGAAGATGCGGTTTCAACA 236

Db 60593 GTGAGTGCACCATGCGCGCTAATTTTGTATGTAAGTGAAGATGCGGTTTCAACA 60652

Qy 237 TTAAGCCGCTGTGTCTTGAATCTCTGACCTCAGGTGATCCACCCCTCAGCTCTTAA 296

Db 60653 TTGGCAGGCTGTGTCTTGAATCTCTGACCTCAGGTGATCCACCCCTTGGCTCCCAA 60712

Qy 297 GTGCTGGATTACAGGATGATGACCGCGCCGCAAGGATGATGTTTAAAGAA 356

Db 60713 GTGCTGGATTACAGGATGATGACCGCGCCGCTAGGCAATATTTTATGAAC 60772

Qy 357 TAATTGAATGTTT 371

Db 60773 TGTCTGAGAAGCTT 60787

RESULT 15

US-09-925-065A-127303

; Sequence 127303, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 127303

; LENGTH: 560

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-925-065A-127303

Query Match 3.0%; Score 181.2; DB 6; Length 560;

Best Local Similarity 82.2%; Pred. No. 5,7e+03;

Matches 222; Conservative 1; Mismatches 39; Indels 8; Gaps 1;

Qy 106 ACCTGAGCTCACTGCAACTCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCTCC 165

Db 59 ATCTGAGCTCACTGCAACTCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCTCC 118

Qy 166 CGCTGAGCTGAGCTACAGC-----GACGCGCGCTAATTTTGTATTTTGTAT 217

Db 119 TGAATGAGCTGAGCTACAGC-----GACGCGCGCTAATTTTGTATTTTGTAT 178

Qy 218 GAGATGGGGTTTCAATATTAGCCGCTGCTGCTTGAATCTCTGAGCTGAGTATCA 277

Db 179 GAGAGGGGGTTTCAATATTAGCCGCTGCTGCTTGAATCTCTGAGCTGAGTATCA 238

Qy 278 CCCAGCTCAAGCTCTTAAGTGTGGATTACAGGATGATGATGATGATGATGATGAT 337

Db 239 CCGAGCTCAAGCTCTTAAGTGTGGATTACAGGATGATGATGATGATGATGATGAT 298

Qy 338 GTCAATTTTATTAAGATTAATTAATG 367

Db 299 TCACATTTTATTAAGATTAATTAATG 328

Search completed: March 24, 2006, 02:39:02
 Job time : 1234 secs